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(54) Title: SINGLE NUCLEOTIDE POLYMORPHISMS AS PREDICTIVE DIAGNOSTICS FOR ADVERSE DRUG REAC-
TIONS (ADR) AND DRUG EFFICACY

(57) Abstract: The invention provides diagnostic methods and kits including oligo and/or polynucleotides or derivatives, including
as well antibodies determining whether a human subject is at risk of getting adverse drug reaction after statin therapy or whether
the human subject is a high or low responder or a good a or bad metabolizer of statins. The invention provides further diagnostic
methods and kits including antibodies determining whether a human subject is at risk for a cardiovascular disease. Still further the
invention provides polymorphic sequences and other genes.

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Single Nucleotide Polymorphisms as Predictive Diagnostics for Adverse Drug Reactions (ADR) and Drug Efficacy

Technical Field

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This invention relates to genetic polymorphisms useful for assessing the response to lipid lowering drug therapy and adverse drug reactions of those medicaments. In addition it relates to genetic polymorphisms useful for assessing cardiovascular risks in humans, including, but not limited to, atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial inflammation, myocardial infarction, and stroke. Specifically, the present invention identifies and describes gene variations which are individually present in humans with cardiovascular disease states, relative to humans with normal, or non-cardiovascular disease states, and/or in response to medications relevant to cardiovascular disease. Further, the present invention provides methods for the identification and therapeutic use of compounds as treatments of cardiovascular disease or as prophylactic therapy for cardiovascular diseases. Moreover, the present invention provides methods for the diagnostic monitoring of patients undergoing clinical evaluation for the treatment of cardiovascular disease, and for monitoring the efficacy of compounds in clinical trials. Still further, the present invention provides methods to use gene variations to predict personal medication schemes omitting adverse drug reactions and allowing an adjustment of the drug dose to achieve maximum benefit for the patient. Additionally, the present invention describes methods for the diagnostic evaluation and prognosis of various cardiovascular diseases, and for the identification of subjects exhibiting a predisposition to such conditions.

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Background of the Invention

Cardiovascular disease is a major health risk throughout the industrialized world.

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Cardiovascular diseases include but are not limited by the following disorders of the heart and the vascular system: congestive heart failure, myocardial infarction,

atherosclerosis, ischemic diseases of the heart, coronary heart disease, all kinds of atrial and ventricular arrhythmias, hypertensive vascular diseases and peripheral vascular diseases.

5 Heart failure is defined as a pathophysiologic state in which an abnormality of cardiac function is responsible for the failure of the heart to pump blood at a rate commensurate with the requirement of the metabolizing tissue. It includes all forms of pumping failure such as high-output and low-output, acute and chronic, right-sided or left-sided, systolic or diastolic, independent of the underlying cause.

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Myocardial infarction (MI) is generally caused by an abrupt decrease in coronary blood flow that follows a thrombotic occlusion of a coronary artery previously narrowed by arteriosclerosis. MI prophylaxis (primary and secondary prevention) is included as well as the acute treatment of MI and the prevention of complications.

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Ischemic diseases are conditions in which the coronary flow is restricted resulting in an perfusion which is inadequate to meet the myocardial requirement for oxygen. This group of diseases include stable angina, unstable angina and asymptomatic ischemia.

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Arrhythmias include all forms of atrial and ventricular tachyarrhythmias (atrial tachycardia, atrial flutter, atrial fibrillation, atrio-ventricular reentrant tachycardia, preexcitation syndrome, ventricular tachycardia, ventricular flutter, ventricular fibrillation) as well as bradycardic forms of arrhythmias.

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Hypertensive vascular diseases include primary as well as all kinds of secondary arterial hypertension (renal, endocrine, neurogenic, others).

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Peripheral vascular diseases are defined as vascular diseases in which arterial and/or venous flow is reduced resulting in an imbalance between blood supply and tissue oxygen demand. It includes chronic peripheral arterial occlusive disease (PAOD),

acute arterial thrombosis and embolism, inflammatory vascular disorders, Raynaud's phenomenon and venous disorders.

5 Atherosclerosis, the most prevalent of vascular diseases, is the principal cause of heart attack, stroke, and gangrene of the extremities, and thereby the principal cause of death. Atherosclerosis is a complex disease involving many cell types and molecular factors (for a detailed review, see Ross, 1993, Nature 362: 801-809 and Luskis, A. J., Nature 407, 233-241 (2000)). The process, in normal circumstances a protective response to insults to the endothelium and smooth muscle cells (SMCs) of the wall of the artery, consists of the formation of fibrofatty and fibrous lesions or plaques, preceded and accompanied by inflammation. The advanced lesions of atherosclerosis may occlude the artery concerned, and result from an excessive inflammatory-fibroproliferative response to numerous different forms of insult. For example, shear stresses are thought to be responsible for the frequent occurrence of atherosclerotic plaques in regions of the circulatory system where turbulent blood flow occurs, such as branch points and irregular structures.

20 The first observable event in the formation of an atherosclerotic plaque occurs when blood-borne monocytes adhere to the vascular endothelial layer and transmigrate through to the sub-endothelial space. Adjacent endothelial cells at the same time produce oxidized low density lipoprotein (LDL). These oxidized LDLs are then taken up in large amounts by the monocytes through scavenger receptors expressed on their surfaces. In contrast to the regulated pathway by which native LDL (nLDL) is taken up by nLDL specific receptors, the scavenger pathway of uptake is not regulated by the monocytes.

30 These lipid-filled monocytes are called foam cells, and are the major constituent of the fatty streak. Interactions between foam cells and the endothelial and SMCs which surround them lead to a state of chronic local inflammation which can eventually lead to smooth muscle cell proliferation and migration, and the formation of a fibrous

plaque. Such plaques occlude the blood vessel concerned and thus restrict the flow of blood, resulting in ischemia.

5 Ischemia is a condition characterized by a lack of oxygen supply in tissues of organs due to inadequate perfusion. Such inadequate perfusion can have number of natural causes, including atherosclerotic or restenotic lesions, anemia, or stroke, to name a few. Many medical interventions, such as the interruption of the flow of blood during bypass surgery, for example, also lead to ischemia. In addition to sometimes being caused by diseased cardiovascular tissue, ischemia may sometimes affect
10 cardiovascular tissue, such as in ischemic heart disease. Ischemia may occur in any organ, however, that is suffering a lack of oxygen supply.

The most common cause of ischemia in the heart is atherosclerotic disease of epicardial coronary arteries. By reducing the lumen of these vessels, atherosclerosis
15 causes an absolute decrease in myocardial perfusion in the basal state or limits appropriate increases in perfusion when the demand for flow is augmented. Coronary blood flow can also be limited by arterial thrombi, spasm, and, rarely, coronary emboli, as well as by ostial narrowing due to luetic aortitis. Congenital abnormalities, such as anomalous origin of the left anterior descending coronary artery from the
20 pulmonary artery, may cause myocardial ischemia and infarction in infancy, but this cause is very rare in adults. Myocardial ischemia can also occur if myocardial oxygen demands are abnormally increased, as in severe ventricular hypertrophy due to hypertension or aortic stenosis. The latter can be present with angina that is indistinguishable from that caused by coronary atherosclerosis. A reduction in the
25 oxygen-carrying capacity of the blood, as in extremely severe anemia or in the presence of carboxy-hemoglobin, is a rare cause of myocardial ischemia. Not infrequently, two or more causes of ischemia will coexist, such as an increase in oxygen demand due to left ventricular hypertrophy and a reduction in oxygen supply secondary to coronary atherosclerosis.

The foregoing studies are aimed at defining the role of particular gene variations presumed to be involved in the misleading of normal cellular function leading to cardiovascular disease. However, such approaches cannot identify the full panoply of gene variations that are involved in the disease process.

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At present, the only available treatments for cardiovascular disorders are pharmaceutical based medications that are not targeted to an individual's actual defect; examples include angiotensin converting enzyme (ACE) inhibitors and diuretics for hypertension, insulin supplementation for non-insulin dependent diabetes mellitus (NIDDM), cholesterol reduction strategies for dyslipidaemia, anticoagulants, β blockers for cardiovascular disorders and weight reduction strategies for obesity. If targeted treatment strategies were available it might be possible to predict the response to a particular regime of therapy and could markedly increase the effectiveness of such treatment. Although targeted therapy requires accurate diagnostic tests for disease susceptibility, once these tests are developed the opportunity to utilize targeted therapy will become widespread. Such diagnostic tests could initially serve to identify individuals at most risk of hypertension and could allow them to make changes in lifestyle or diet that would serve as preventative measures. The benefits associated by coupling the diagnostic tests with a system of targeted therapy could include the reduction in dosage of administered drugs and thus the amount of unpleasant side effects suffered by an individual. In more severe cases a diagnostic test may suggest that earlier surgical intervention would be useful in preventing a further deterioration in condition.

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It is an object of the invention to provide genetic diagnosis of predisposition or susceptibility for cardiovascular diseases. Another related object is to provide treatment to reduce or prevent or delay the onset of disease in those predisposed or susceptible to this disease. A further object is to provide means for carrying out this diagnosis.

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Accordingly, a first aspect of the invention provides a method of diagnosis of disease in an individual, said method comprising determining one, various or all genotypes in said individual of the genes listed in the Examples.

5 In another aspect, the invention provides a method of identifying an individual predisposed or susceptible to a disease, said method comprising determining one, various or all genotypes in said individual of the genes listed in the Examples.

10 The invention is of advantage in that it enables diagnosis of a disease or of certain disease states via genetic analysis which can yield useable results before onset of disease symptoms, or before onset of severe symptoms. The invention is further of advantage in that it enables diagnosis of predisposition or susceptibility to a disease or of certain disease states via genetic analysis.

15 The invention may also be of use in confirming or corroborating the results of other diagnostic methods. The diagnosis of the invention may thus suitably be used either as an isolated technique or in combination with other methods and apparatus for diagnosis, in which latter case the invention provides a further test on which a diagnosis may be assessed.

20 The present invention stems from using allelic association as a method for genotyping individuals; allowing the investigation of the molecular genetic basis for cardiovascular diseases. In a specific embodiment the invention tests for the polymorphisms in the sequences of the listed genes in the Examples. The invention demonstrates a link between this polymorphisms and predispositions to cardiovascular diseases by showing that allele frequencies significantly differ when individuals with "bad" serum lipids are compared to individuals with "good" serum levels. The meaning of "good and bad" serum lipid levels is defined in Table 1a.

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30 Certain disease states would benefit, that is to say the suffering of the patient may be reduced or prevented or delayed, by administration of treatment or therapy in

advance of disease appearance; this can be more reliably carried out if advance diagnosis of predisposition or susceptibility to disease can be diagnosed.

Pharmacogenomics and adverse drug reactions

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Adverse drug reactions (ADRs) remain a major clinical problem. A recent meta-analysis suggested that in the USA in 1994, ADRs were responsible for 100 000 deaths, making them between the fourth and sixth commonest cause of death (Lazarou 1998, J. Am. Med. Assoc. 279:1200). Although these figures have been heavily criticized, they emphasize the importance of ADRs. Indeed, there is good evidence that ADRs account for 5% of all hospital admissions and increase the length of stay in hospital by two days at an increased cost of ~\$2500 per patient. ADRs are also one of the commonest causes of drug withdrawal, which has enormous financial implications for the pharmaceutical industry. ADRs, perhaps fortunately, only affect a minority of those taking a particular drug. Although factors that determine susceptibility are unclear in most cases, there is increasing interest in the role of genetic factors. Indeed, the role of inheritable variations in predisposing patients to ADRs has been appreciated since the late 1950s and early 1960s through the discovery of deficiencies in enzymes such as pseudocholinesterase (butyrylcholinesterase) and glucose-6-phosphate dehydrogenase (G6PD). More recently, with the first draft of the human genome just completed, there has been renewed interest in this area with the introduction of terms such as pharmacogenomics and toxicogenomics. Essentially, the aim of pharmacogenomics and pharmacogenetics is to produce personalized medicines, whereby administration of the drug class and dosage is tailored to an individual genotype. Thus, the term pharmacogenetics embraces both efficacy and toxicity.

The 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase inhibitors ("statins") specifically inhibit the enzyme HMG-CoA reductase which catalyzes the rate limiting step in cholesterol biosynthesis. These drugs are effective in reducing the primary and secondary risk of coronary artery disease and coronary events, such

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as heart attack, in middle-aged and older men and women, in both diabetic and non-diabetic patients, and are often prescribed for patients with hyperlipidemia. Statins used in secondary prevention of coronary artery or heart disease significantly reduce the risk of stroke, total mortality and morbidity and attacks of myocardial ischemia; the use of statins is also associated with improvements in endothelial and fibrinolytic functions and decreased platelet thrombus formation.

The tolerability of these drugs during long term administration is an important issue. Adverse reactions involving skeletal muscle are not uncommon, and sometimes serious adverse reactions involving skeletal muscle such as myopathy and rhabdomyolysis may occur, requiring discontinuation of the drug. In addition an increase in serum creatine kinase (CK) may be a sign of a statin related adverse event. The extend of such adverse events can be read from the extend of the CK level increase (as compared to the upper limit of normal [ULN]).

Occasionally arthralgia, alone or in association with myalgia, has been reported. Also an elevation of liver transaminases has been associated with statin administration.

It was shown that the drug response to statin therapy is a class effects, i.e. all known and presumably also all so far undiscovered statins share the same beneficial and harmful effects (Ucar, M. et al., Drug Safety 2000, 22:441). It follows that the discovery of diagnostic tools to predict the drug response to a single statin will also be of aid to guide therapy with other statins.

The present invention provides diagnostic tests to predict the patient's individual response to statin therapy. Such responses include, but are not limited by the extent of adverse drug reactions, the level of lipid lowering or the drug's influence on disease states. Those diagnostic tests may predict the response to statin therapy either alone or in combination with another diagnostic test or another drug regimen.

Detailed Description of the Invention

The present invention is based at least in part on the discovery that a specific allele of a polymorphic region of a so called "candidate gene" (as defined below) is associated
5 with CVD or drug response.

For the present invention the following candidate genes were analyzed:

- 10 - Genes found to be expressed in cardiac tissue (Hwang et al., Circulation 1997, 96:4146-4203).
- Genes from the following metabolic pathways and their regulatory elements:

Lipid metabolism

15 Numerous studies have shown a connection between serum lipid levels and cardiovascular diseases. Candidate genes falling into this group include but are not limited by genes of the cholesterol pathway, apolipoproteins and their modifying factors.

20 **Coagulation**

Ischemic diseases of the heart and in particular myocardial infarction may be caused by a thrombotic occlusion. Genes falling into this group include all genes of the coagulation cascade and their regulatory elements.

25

Inflammation

Complications of atherosclerosis are the most common causes of death in Western societies. In broad outline atherosclerosis can be considered to be a form of chronic
30 inflammation resulting from interaction modified lipoproteins, monocyte-derived macrophages, T cells, and the normal cellular elements of the arterial wall. This

inflammatory process can ultimately lead to the development of complex lesions, or plaques, that protrude into the arterial lumen. Finally plaque rupture and thrombosis result in the acute clinical complications of myocardial infarction and stroke (Glass et al., Cell 2001, 104:503-516).

5

It follows that all genes related to inflammatory processes, including but not limited by cytokines, cytokine receptors and cell adhesion molecules are candidate genes for CVD.

10 **Glucose and energy metabolism**

As glucose and energy metabolism is interdependent with the metabolism of lipids (see above) also the former pathways contain candidate genes. Energy metabolism in general also relates to obesity, which is an independent risk factor for CVD (Melanson et al., Cardiol Rev 2001 9:202-207). In addition high blood glucose levels are associated with many microvascular and macrovascular complications and may therefore affect an individuals disposition to CVD (Duckworth, Curr Atheroscler Rep 2001, 3:383-391).

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20 **Hypertension**

As hypertension is an independent risk factor for CVD, also genes that are involved in the regulation of systolic and diastolic blood pressure affect an individuals risk for CVD (Safar, Curr Opin Cardiol 2000, 15:258-263). Interestingly hypertension and diabetes (see above) appear to be interdependent, since hypertension is approximately twice as frequent in patients with diabetes compared with patients without the disease. Conversely, recent data suggest that hypertensive persons are more predisposed to the development of diabetes than are normotensive persons (Sowers et al., Hypertension 2001, 37:1053-1059).

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Genes related to drug response

Those genes include metabolic pathways involved in the absorption, distribution, metabolism, excretion and toxicity (ADMET) of drugs. Prominent members of this group are the cytochrome P450 proteins which catalyze many reactions involved in drug metabolism.

Unclassified genes

As stated above, the mechanisms that lead to cardiovascular diseases or define the patient's individual response to drugs are not completely elucidated. Hence also candidate genes were analysed, which could not be assigned to the above listed categories. The present invention is based at least in part on the discovery of polymorphisms, that lie in genomic regions of unknown physiological function.

Results

After conducting an association study, we surprisingly found polymorphic sites in a number of candidate genes which show a strong correlation with the following phenotypes of the patients analysed: "Healthy" as used herein refers to individuals that neither suffer from existing CVD, nor exhibit an increased risk for CVD through their serum lipid level profile. "CVD prone" as used herein refers to individuals with existing CVD and/or a serum lipid profile that confers a high risk to get CVD (see Table 1a for definitions of healthy and CVD prone serum lipid levels). "High responder" as used herein refers to patients who benefit from relatively small amounts of a given drug. "Low responder" as used herein refers to patients who need relatively high doses in order to obtain benefit from the medication. "Tolerant patient" refers to individuals who can tolerate high doses of a medicament without exhibiting adverse drug reactions. "ADR patient" as used herein refers to individuals who suffer from ADR or show clinical symptoms (like creatine kinase elevation in

blood) even after receiving only minor doses of a medicament (see Table 1b for a detailed definition of drug response phenotypes).

5 Polymorphic sites in candidate genes that were found to be significantly associated with either of the above mentioned phenotypes will be referred to as "phenotype associated SNPs" (PA SNPs). The respective genomic loci that harbour PA SNPs will be referred to as "phenotype associated genes" (PA genes), irrespective of the actual function of this gene locus.

10 As PA SNPs are linked to other SNPs in neighboring genes on a chromosome (Linkage Disequilibrium) those SNPs could also be used as marker SNPs. In a recent publication it was shown that SNPs are linked over 100 kb in some cases more than 150 kb (Reich D.E. et al. Nature 411, 199-204, 2001). Hence SNPs lying in regions neighbouring PA SNPs could be linked to the latter and by this being a diagnostic
15 marker. These associations could be performed as described for the gene polymorphism in methods.

Definitions

20 For convenience, the meaning of certain terms and phrases employed in the specification, examples, and appended claims are provided below. Moreover, the definitions by itself are intended to explain a further background of the invention.

The term "allele", which is used interchangeably herein with "allelic variant" refers
25 to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for the gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several
30 nucleotides, and can include substitutions, deletions, and insertions of nucleotides. An allele of a gene can also be a form of a gene containing a mutation.

The term "allelic variant of a polymorphic region of a gene" refers to a region of a gene having one of several nucleotide sequences found in that region of the gene in other individuals.

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"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40% identity, though preferably less than 25% identity, with one of the sequences of the present invention.

15

The term "a homologue of a nucleic acid" refers to a nucleic acid having a nucleotide sequence having a certain degree of homology with the nucleotide sequence of the nucleic acid or complement thereof. A homologue of a double stranded nucleic acid having SEQ ID NO. X is intended to include nucleic acids having a nucleotide sequence which has a certain degree of homology with SEQ ID NO. X or with the complement thereof. Preferred homologous of nucleic acids are capable of hybridizing to the nucleic acid or complement thereof.

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The term "interact" as used herein is meant to include detectable interactions between molecules, such as can be detected using, for example, a hybridization assay.

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The term interact is also meant to include "binding" interactions between molecules. Interactions may be, for example, protein-protein, protein-nucleic acid, protein-small molecule or small molecule-nucleic acid in nature.

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The term "intronic sequence" or "intronic nucleotide sequence" refers to the nucleotide sequence of an intron or portion thereof.

5 The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs or RNAs, respectively, that are present in the natural source of the macromolecule. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized.

10

Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and

15 recombinant polypeptides.

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The term "lipid" shall refer to a fat or fat-like substance that is insoluble in polar solvents such as water. The term "lipid" is intended to include true fats (e.g. esters of fatty acids and glycerol); lipids (phospholipids, cerebrosides, waxes); sterols (cholesterol, ergosterol) and lipoproteins (e.g. HDL, LDL and VLDL).

The term "locus" refers to a specific position in a chromosome. For example, a locus of a gene refers to the chromosomal position of the gene.

25 The term "modulation" as used herein refers to both up-regulation, (i.e., activation or stimulation), for example by agonizing, and down-regulation (i.e. inhibition or suppression), for example by antagonizing of a bioactivity (e.g. expression of a gene).

30 The term "molecular structure" of a gene or a portion thereof refers to the structure as defined by the nucleotide content (including deletions, substitutions, additions of one

or more nucleotides), the nucleotide sequence, the state of methylation, and/or any other modification of the gene or portion thereof.

5 The term "mutated gene" refers to an allelic form of a gene, which is capable of altering the phenotype of a subject having the mutated gene relative to a subject which does not have the mutated gene. If a subject must be homozygous for this mutation to have an altered phenotype, the mutation is said to be recessive. If one copy of the mutated gene is sufficient to alter the genotype of the subject, the mutation is said to be dominant. If a subject has one copy of the mutated gene and
10 has a phenotype that is intermediate between that of a homozygous and that of a heterozygous (for that gene) subject, the mutation is said to be co-dominant.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term
15 should also be understood to include, as equivalents, derivatives, variants and analogs of either RNA or DNA made from nucleotide analogs, including peptide nucleic acids (PNA), morpholino oligonucleotides (J. Summerton and D. Weller, Antisense and Nucleic Acid Drug Development 7:187 (1997)) and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded
20 polynucleotides. Deoxyribonucleotides include deoxyadenosine, deoxycytidine, deoxyguanosine, and deoxythymidine. For purposes of clarity, when referring herein to a nucleotide of a nucleic acid, which can be DNA or an RNA, the term "adenosine", "cytidine", "guanosine", and "thymidine" are used. It is understood that if the nucleic acid is RNA, a nucleotide having a uracil base is uridine.

25 The term "nucleotide sequence complementary to the nucleotide sequence set forth in SEQ ID NO. x" refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having SEQ ID NO. x. The term "complementary strand" is used herein interchangeably with the term "complement". The complement of a nucleic
30 acid strand can be the complement of a coding strand or the complement of a non-coding strand. When referring to double stranded nucleic acids, the complement of a

nucleic acid having SEQ ID NO. x refers to the complementary strand of the strand having SEQ ID NO. x or to any nucleic acid having the nucleotide sequence of the complementary strand of SEQ ID NO. x. When referring to a single stranded nucleic acid having the nucleotide sequence SEQ ID NO. x, the complement of this nucleic acid is a nucleic acid having a nucleotide sequence which is complementary to that of SEQ ID NO. x. The nucleotide sequences and complementary sequences thereof are always given in the 5' to 3' direction. The term "complement" and "reverse complement" are used interchangeably herein.

10 The term "operably linked" is intended to mean that the promoter is associated with the nucleic acid in such a manner as to facilitate transcription of the nucleic acid.

The term "polymorphism" refers to the coexistence of more than one form of a gene or portion thereof. A portion of a gene of which there are at least two different forms, i.e., two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

20 To describe a "polymorphic site" in a nucleotide sequence often there is used an "ambiguity code" that stands for the possible variations of nucleotides in one site. The list of ambiguity codes is summarized in the following table:

- 17 -

Ambiguity (IUPAC Nomenclature)	Codes
B	c/g/t
D	a/g/t
H	a/c/t
K	g/t
M	a/c
N	a/c/g/t
R	a/g
S	c/g
V	a/c/g
W	a/t
Y	c/t

So, for example, a "R" in a nucleotide sequence means that either an "a" or a "g" could be at that position.

- 5 The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

10 A "regulatory element", also termed herein "regulatory sequence" is intended to include elements which are capable of modulating transcription from a basic promoter and include elements such as enhancers and silencers. The term "enhancer", also referred to herein as "enhancer element", is intended to include regulatory elements capable of increasing, stimulating, or enhancing transcription from a basic promoter. The term "silencer", also referred to herein as "silencer element" is intended to include regulatory elements capable of decreasing, inhibiting, or repressing transcription from a basic promoter. Regulatory elements are typically present in 5' flanking regions of genes. However, regulatory elements have also been shown to be present in other regions of a gene, in particular in introns. Thus, it is possible that genes have regulatory elements located in introns, exons, coding

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regions, and 3' flanking sequences. Such regulatory elements are also intended to be encompassed by the present invention and can be identified by any of the assays that can be used to identify regulatory elements in 5' flanking regions of genes.

5 The term "regulatory element" further encompasses "tissue specific" regulatory elements, i.e., regulatory elements which effect expression of the selected DNA sequence preferentially in specific cells (e.g., cells of a specific tissue). gene expression occurs preferentially in a specific cell if expression in this cell type is significantly higher than expression in other cell types. The term "regulatory
10 element" also encompasses non-tissue specific regulatory elements, i.e., regulatory elements which are active in most cell types. Furthermore, a regulatory element can be a constitutive regulatory element, i.e., a regulatory element which constitutively regulates transcription, as opposed to a regulatory element which is inducible, i.e., a regulatory element which is active primarily in response to a stimulus. A stimulus
15 can be, e.g., a molecule, such as a hormone, cytokine, heavy metal, phorbol ester, cyclic AMP (cAMP), or retinoic acid.

Regulatory elements are typically bound by proteins, e.g., transcription factors. The term "transcription factor" is intended to include proteins or modified forms thereof,
20 which interact preferentially with specific nucleic acid sequences, i.e., regulatory elements, and which in appropriate conditions stimulate or repress transcription. Some transcription factors are active when they are in the form of a monomer. Alternatively, other transcription factors are active in the form of a dimer consisting of two identical proteins or different proteins (heterodimer). Modified forms of
25 transcription factors are intended to refer to transcription factors having a post-translational modification, such as the attachment of a phosphate group. The activity of a transcription factor is frequently modulated by a post-translational modification. For example, certain transcription factors are active only if they are phosphorylated on specific residues. Alternatively, transcription factors can be active in the absence
30 of phosphorylated residues and become inactivated by phosphorylation. A list of

- 19 -

known transcription factors and their DNA binding site can be found, e.g., in public databases, e.g., TFMATRIX Transcription Factor Binding Site Profile database.

5 As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least approximately 6, 12, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130 or 140 consecutive nucleotides of either strand of a gene.

10 The term "wild-type allele" refers to an allele of a gene which, when present in two copies in a subject results in a wild-type phenotype. There can be several different wild-type alleles of a specific gene, since certain nucleotide changes in a gene may not affect the phenotype of a subject having two copies of the gene with the nucleotide changes.

15 "Adverse drug reaction" (ADR) as used herein refers to an appreciably harmful or unpleasant reaction, resulting from an intervention related to the use of a medicinal product, which predicts hazard from future administration and warrants prevention or specific treatment, or alteration of the dosage regimen, or withdrawal of the product. In its most severe form an ADR might lead to the death of an individual.

20 The term "Drug Response" is intended to mean any response that a patient exhibits upon drug administration. Specifically drug response includes beneficial, i.e. desired drug effects, ADR or no detectable reaction at all. More specifically the term drug response could also have a qualitative meaning, i.e. it embraces low or high
25 beneficial effects, respectively and mild or severe ADR, respectively. The term "Statin Response" as used herein refers to drug response after statin administration. An individual drug response includes also a good or bad metabolizing of the drug, meaning that "bad metabolizers" accumulate the drug in the body and by this could show side effects of the drug due to accumulative overdoses.

30

"Candidate gene" as used herein includes genes that can be assigned to either normal cardiovascular function or to metabolic pathways that are related to onset and/or progression of cardiovascular diseases.

5 With regard to drug response the term "candidate gene" includes genes that can be assigned to distinct phenotypes regarding the patient's response to drug administration. Those phenotypes may include patients who benefit from relatively small amounts of a given drug (high responders) or patients who need relatively high doses in order to obtain the same benefit (low responders). In addition those
10 phenotypes may include patients who can tolerate high doses of a medicament without exhibiting ADR, or patients who suffer from ADR even after receiving only low doses of a medicament.

As neither the development of cardiovascular diseases nor the patient's response to
15 drug administration is completely understood, the term "candidate gene" may also comprise genes with presently unknown function.

"PA SNP" (phenotype associated SNP) refers to a polymorphic site which shows a significant association with a patients phenotype (healthy, diseased, low or high
20 responder, drug tolerant, ADR prone, etc.)

"PA gene" (phenotype associated gene) refers to a genomic locus harbouring a PA SNP, irrespective of the actual function of this gene locus.

25 PA gene polypeptide refers to a polypeptide encoded at least in part by a PA gene.

The term "Secondary SNP" is intended to mean a SNP that is in neighborhood to at least one other ("primary") SNP. Due to linkage disequilibrium both primary and secondary SNP(s) might shown a similar association with a phenotype.

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The term "Haplotype" as used herein refers to a group of two or more SNPs that are functionally and/or spatially linked. I.e. haplotypes define groups of SNPs that lie inside genes belonging to identical (or related metabolic) pathways and/or lie on the same chromosome. Haplotypes are expected to give better predictive/diagnostic
5 information than a single SNP

The term "statin" is intended to embrace all inhibitors of the enzyme 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) reductase. Statins specifically inhibit the enzyme HMG-CoA reductase which catalyzes the rate limiting step in cholesterol
10 biosynthesis. Known statins are Atorvastatin, Cerivastatin, Fluvastatin, Lovastatin, Pravastatin and Simvastatin.

Methods for Assessing Cardiovascular Status

15 The present invention provides diagnostic methods for assessing cardiovascular status in a human individual. Cardiovascular status as used herein refers to the physiological status of an individual's cardiovascular system as reflected in one or more markers or indicators. Status markers include without limitation clinical measurements such as, e.g., blood pressure, electrocardiographic profile, and
20 differentiated blood flow analysis as well as measurements of LDL- and HDL-Cholesterol levels, other lipids and other well established clinical parameters that are standard in the art. Status markers according to the invention include diagnoses of one or more cardiovascular syndromes, such as, e.g., hypertension, acute myocardial infarction, silent myocardial infarction, stroke, and atherosclerosis. It will be
25 understood that a diagnosis of a cardiovascular syndrome made by a medical practitioner encompasses clinical measurements and medical judgement. Status markers according to the invention are assessed using conventional methods well known in the art. Also included in the evaluation of cardiovascular status are quantitative or qualitative changes in status markers with time, such as would be
30 used, e.g., in the determination of an individual's response to a particular therapeutic regimen.

The methods are carried out by the steps of:

- 5 (i) determining the sequence of one or more polymorphic positions within one, several or all of the genes listed in Examples or other genes mentioned in this file in the individual to establish a polymorphic pattern for the individual; and
- 10 (ii) comparing the polymorphic pattern established in (i) with the polymorphic patterns of humans exhibiting different markers of cardiovascular status. The polymorphic pattern of the individual is, preferably, highly similar and, most preferably, identical to the polymorphic pattern of individuals who exhibit particular status markers, cardiovascular syndromes, and/or particular patterns of response to therapeutic interventions. Polymorphic patterns may also include polymorphic positions in other genes which are shown, in combination with one or more polymorphic positions in the genes listed in the Examples, to correlate with the presence of particular status markers. In one embodiment, the method involves comparing an individual's polymorphic pattern with polymorphic patterns of individuals who have been shown to respond positively or negatively to a particular therapeutic regimen. Therapeutic regimen as used herein refers to treatments aimed at the elimination or amelioration of symptoms and events associated cardiovascular disease. Such treatments include without limitation one or more of alteration in diet, lifestyle, and exercise regimen; invasive and noninvasive surgical techniques such as atherectomy, angioplasty, and coronary bypass surgery; and pharmaceutical interventions, such as administration of ACE inhibitors, angiotensin II receptor antagonists, diuretics, alpha-adrenoreceptor antagonists, cardiac glycosides, phosphodiesterase inhibitors, beta-adrenoreceptor antagonists, calcium channel blockers, HMG-CoA reductase inhibitors, imidazoline receptor blockers, endothelin receptor blockers, organic nitrites, and modulators of protein function of genes listed in the Examples. Interventions with pharmaceutical agents not yet known whose activity
- 15
- 20
- 25
- 30

correlates with particular polymorphic patterns associated with cardiovascular disease are also encompassed. It is contemplated, for example, that patients who are candidates for a particular therapeutic regimen will be screened for polymorphic patterns that correlate with responsivity to that particular regimen.

In a preferred embodiment, the method involves comparing an individual's polymorphic pattern with polymorphic patterns of individuals who exhibit or have exhibited one or more markers of cardiovascular disease, such as, e.g., elevated LDL-Cholesterol levels, high blood pressure, abnormal electrocardiographic profile, myocardial infarction, stroke, or atherosclerosis.

In another embodiment, the method involves comparing an individual's polymorphic pattern with polymorphic patterns of individuals who exhibit or have exhibited one or more drug related phenotypes, such as, e.g., low or high drug response, or adverse drug reactions.

In practicing the methods of the invention, an individual's polymorphic pattern can be established by obtaining DNA from the individual and determining the sequence at predetermined polymorphic positions in the genes such as those described in this file.

The DNA may be obtained from any cell source. Non-limiting examples of cell sources available in clinical practice include blood cells, buccal cells, cervicovaginal cells, epithelial cells from urine, fetal cells, or any cells present in tissue obtained by biopsy. Cells may also be obtained from body fluids, including without limitation blood, saliva, sweat, urine, cerebrospinal fluid, feces, and tissue exudates at the site of infection or inflammation. DNA is extracted from the cell source or body fluid using any of the numerous methods that are standard in the art. It will be understood that the particular method used to extract DNA will depend on the nature of the source.

Diagnostic and Prognostic Assays

5 The present invention provides methods for determining the molecular structure of at least one polymorphic region of a gene, specific allelic variants of said polymorphic region being associated with cardiovascular disease. In one embodiment, determining the molecular structure of a polymorphic region of a gene comprises determining the identity of the allelic variant. A polymorphic region of a gene, of which specific alleles are associated with cardiovascular disease can be located in an exon, an
10 intron, at an intron/exon border, or in the promoter of the gene.

The invention provides methods for determining whether a subject has, or is at risk, of developing a cardiovascular disease. Such disorders can be associated with an aberrant gene activity, e.g., abnormal binding to a form of a lipid, or an aberrant gene
15 protein level. An aberrant gene protein level can result from an aberrant transcription or post-transcriptional regulation. Thus, allelic differences in specific regions of a gene can result in differences of gene protein due to differences in regulation of expression. In particular, some of the identified polymorphisms in the human gene may be associated with differences in the level of transcription, RNA maturation,
20 splicing, or translation of the gene or transcription product.

In preferred embodiments, the methods of the invention can be characterized as comprising detecting, in a sample of cells from the subject, the presence or absence of a specific allelic variant of one or more polymorphic regions of a gene. The allelic
25 differences can be: (i) a difference in the identity of at least one nucleotide or (ii) a difference in the number of nucleotides, which difference can be a single nucleotide or several nucleotides.

A preferred detection method is allele specific hybridization using probes
30 overlapping the polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the polymorphic region. Examples of probes for detecting specific allelic

variants of the polymorphic region located in intron X are probes comprising a nucleotide sequence set forth in any of SEQ ID NO. X. In a preferred embodiment of the invention, several probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip". Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides (GeneChip, Affymetrix). Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) Human Mutation 7:244 and in Kozal et al. (1996) Nature Medicine 2:753. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment. For example, the identity of the allelic variant of the nucleotide polymorphism of nucleotide A or G at position 33 of Seq ID 1 (baySNP179) and that of other possible polymorphic regions can be determined in a single hybridization experiment.

In other detection methods, it is necessary to first amplify at least a portion of a gene prior to identifying the allelic variant. Amplification can be performed, e.g., by PCR and/or LCR, according to methods known in the art. In one embodiment, genomic DNA of a cell is exposed to two PCR primers and amplification for a number of cycles sufficient to produce the required amount of amplified DNA. In preferred embodiments, the primers are located between 40 and 350 base pairs apart. Preferred primers for amplifying gene fragments of genes of this file are listed in Table 2 in the Examples.

Alternative amplification methods include: self sustained sequence replication (Guatelli, J. C. et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:1874-1878), transcriptional amplification system (Kwoh, D. Y. et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:1173-1177), Q-Beta Replicase (Lizardi, P. M. et al., 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method, followed

by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

5 In one embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence at least a portion of a gene and detect allelic variants, e.g., mutations, by comparing the sequence of the sample sequence with the corresponding wild-type (control) sequence. Exemplary sequencing reactions include those based on techniques developed by Maxam and Gilbert (Proc. Natl Acad Sci
10 USA (1977) 74:560) or Sanger (Sanger et al (1977) Proc. Nat. Acad. Sci 74:5463). It is also contemplated that any of a variety of automated sequencing procedures may be utilized when performing the subject assays (Biotechniques (1995) 19:448), including sequencing by mass spectrometry (see, for example, U.S. Pat. No. 5,547,835 and international patent application Publication Number WO 94/16101,
15 entitled DNA Sequencing by Mass Spectrometry by H. Koster; U.S. Pat. No. 5,547,835 and international patent application Publication Number WO 94/21822 entitled "DNA Sequencing by Mass Spectrometry Via Exonuclease Degradation" by H. Koster), and U.S. Pat. No. 5,605,798 and International Patent Application No. PCT/US96/03651 entitled DNA Diagnostics Based on Mass Spectrometry by H.
20 Koster; Cohen et al. (1996) Adv Chromatogr 36:127-162; and Griffin et al. (1993) Appl Biochem Biotechnol 38:147-159). It will be evident to one skilled in the art that, for certain embodiments, the occurrence of only one, two or three of the nucleic acid bases need be determined in the sequencing reaction. For instance, A-track or the like, e.g., where only one nucleotide is detected, can be carried out.

25

Yet other sequencing methods are disclosed, e.g., in U.S. Pat. No. 5,580,732 entitled "Method of DNA sequencing employing a mixed DNA-polymer chain probe" and U.S. Pat. No. 5,571,676 entitled "Method for mismatch-directed in vitro DNA sequencing".

30

In some cases, the presence of a specific allele of a gene in DNA from a subject can be shown by restriction enzyme analysis. For example, a specific nucleotide polymorphism can result in a nucleotide sequence comprising a restriction site which is absent from the nucleotide sequence of another allelic variant.

5

In other embodiments, alterations in electrophoretic mobility is used to identify the type of gene allelic variant. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al. (1989) Proc Natl. Acad. Sci USA 86:2766, see also Cotton (1993) Mutat Res 285:125-144; and Hayashi (1992) Genet Anal Tech Appl 9:73-79). Single-stranded DNA fragments of sample and control nucleic acids are denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In another preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al. (1991) Trends Genet 7:5).

20

In yet another embodiment, the identity of an allelic variant of a polymorphic region is obtained by analyzing the movement of a nucleic acid comprising the polymorphic region in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al (1985) Nature 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) Biophys Chem 265:1275).

25

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Examples of techniques for detecting differences of at least one nucleotide between 2 nucleic acids include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide probes may be prepared in which the known polymorphic nucleotide is placed centrally (allele-specific probes) and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki et al. (1986) Nature 324:163); Saiki et al (1989) Proc. Natl Acad. Sci USA 86:6230; and Wallace et al. (1979) Nucl. Acids Res. 6:3543). Such allele specific oligonucleotide hybridization techniques may be used for the simultaneous detection of several nucleotide changes in different polymorphic regions of gene. For example, oligonucleotides having nucleotide sequences of specific allelic variants are attached to a hybridizing membrane and this membrane is then hybridized with labeled sample nucleic acid. Analysis of the hybridization signal will then reveal the identity of the nucleotides of the sample nucleic acid.

Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used. Oligonucleotides used as primers for specific amplification may carry the allelic variant of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al (1989) Nucleic Acids Res. 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) Tibtech 11:238; Newton et al. (1989) Nucl. Acids Res. 17:2503). This technique is also termed "PROBE" for Probe Oligo Base Extension. In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al (1992) Mol. Cell Probes 6:1).

In another embodiment, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, e.g., in U.S. Pat. No. 4,998,617 and in Landegren, U. et al., Science 241:1077-1080 (1988). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting

sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g., biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin, or another biotin ligand. Nickerson, D. A. et al. have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, D. A. et al., Proc. Natl. Acad. Sci. (U.S.A.) 87:8923-8927 (1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Several techniques based on this OLA method have been developed and can be used to detect specific allelic variants of a polymorphic region of a gene. For example, U.S. Pat. No. 5,593,826 discloses an OLA using an oligonucleotide having 3'-amino group and a 5'-phosphorylated oligonucleotide to form a conjugate having a phosphoramidate linkage. In another variation of OLA described in Tobe et al. ((1996)Nucleic Acids Res 24: 3728), OLA combined with PCR permits typing of two alleles in a single microtiter well. By marking each of the allele-specific primers with a unique hapten, i.e. digoxigenin and fluorescein, each LA reaction can be detected by using hapten specific antibodies that are labeled with different enzyme reporters, alkaline phosphatase or horseradish peroxidase. This system permits the detection of the two alleles using a high throughput format that leads to the production of two different colors.

The invention further provides methods for detecting single nucleotide polymorphisms in a gene. Because single nucleotide polymorphisms constitute sites of variation flanked by regions of invariant sequence, their analysis requires no more than the determination of the identity of the single nucleotide present at the site of variation and it is unnecessary to determine a complete gene sequence for each patient. Several methods have been developed to facilitate the analysis of such single nucleotide polymorphisms.

In one embodiment, the single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in Mundy, C. R. (U.S. Pat. No. 4,656,127). According to the method, a primer complementary to the allelic sequence immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was complementary to that of the nucleotide derivative used in the reaction. This method has the advantage that it does not require the determination of large amounts of extraneous sequence data.

In another embodiment of the invention, a solution-based method is used for determining the identity of the nucleotide of a polymorphic site. Cohen, D. et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

An alternative method, known as Genetic Bit Analysis or GBA™ is described by Goelet, P. et al. (PCT Appln. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087) the method of Goelet, P. et

al. is preferably a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

5 Recently, several primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-7784 (1989); Sokolov, B. P., Nucl. Acids Res. 18:3671 (1990); Syvanen, A. -C., et al., Genomics 8:684-692 (1990), Kuppuswamy, M. N. et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147 (1991); Prezant, T. R. et al., Hum. Mutat. 1:159-164 (1992); Ugozzoli, L. et al., GATA 9:107-112 (1992); Nyren, P. et al., Anal. Biochem. 208:171-175 (1993)). These methods differ from GBATM in
10 that they all rely on the incorporation of labeled deoxynucleotides to discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are proportional to the length of the run
15 (Syvanen, A.-C., et al., Amer. J. Hum. Genet. 52:46-59 (1993)).

For determining the identity of the allelic variant of a polymorphic region located in the coding region of a gene, yet other methods than those described above can be used. For example, identification of an allelic variant which encodes a mutated gene
20 protein can be performed by using an antibody specifically recognizing the mutant protein in, e.g., immunohistochemistry or immunoprecipitation. Antibodies to wild-type gene protein are described, e.g., in Acton et al. (1999) Science 271:518 (anti-mouse gene antibody cross-reactive with human gene). Other antibodies to wild-type gene or mutated forms of gene proteins can be prepared according to methods known
25 in the art. Alternatively, one can also measure an activity of an gene protein, such as binding to a lipid or lipoprotein. Binding assays are known in the art and involve, e.g., obtaining cells from a subject, and performing binding experiments with a labeled lipid, to determine whether binding to the mutated form of the receptor differs from binding to the wild-type of the receptor.

If a polymorphic region is located in an exon, either in a coding or non-coding region of the gene, the identity of the allelic variant can be determined by determining the molecular structure of the mRNA, pre-mRNA, or cDNA. The molecular structure can be determined using any of the above described methods for determining the molecular structure of the genomic DNA, e.g., sequencing and SSCP.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits, such as those described above, comprising at least one probe or primer nucleic acid described herein, which may be conveniently used, e.g., to determine whether a subject has or is at risk of developing a disease associated with a specific gene allelic variant.

Sample nucleic acid for using in the above-described diagnostic and prognostic methods can be obtained from any cell type or tissue of a subject. For example, a subject's bodily fluid (e.g. blood) can be obtained by known techniques (e.g. venipuncture) or from human tissues like heart (biopsies, transplanted organs). Alternatively, nucleic acid tests can be performed on dry samples (e.g. hair or skin). Fetal nucleic acid samples for prenatal diagnostics can be obtained from maternal blood as described in International Patent Application No. WO91/07660 to Bianchi. Alternatively, amniocytes or chorionic villi may be obtained for performing prenatal testing.

Diagnostic procedures may also be performed in situ directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents may be used as probes and/or primers for such in situ procedures (see, for example, Nuovo, G. J., 1992, PCR in situ hybridization: protocols and applications, Raven Press, New York).

In addition to methods which focus primarily on the detection of one nucleic acid sequence, profiles may also be assessed in such detection schemes. Fingerprint

profiles may be generated, for example, by utilizing a differential display procedure, Northern analysis and/or RT-PCR.

5 In practicing the present invention, the distribution of polymorphic patterns in a large number of individuals exhibiting particular markers of cardiovascular status or drug response is determined by any of the methods described above, and compared with the distribution of polymorphic patterns in patients that have been matched for age, ethnic origin, and/or any other statistically or medically relevant parameters, who exhibit quantitatively or qualitatively different status markers. Correlations are
10 achieved using any method known in the art, including nominal logistic regression, chi square tests or standard least squares regression analysis. In this manner, it is possible to establish statistically significant correlations between particular polymorphic patterns and particular cardiovascular statuses (given in p values). It is further possible to establish statistically significant correlations between particular
15 polymorphic patterns and changes in cardiovascular status or drug response such as, would result, e.g., from particular treatment regimens. In this manner, it is possible to correlate polymorphic patterns with responsivity to particular treatments.

20 In another embodiment of the present invention two or more polymorphic regions are combined to define so called 'haplotypes'. Haplotypes are groups of two or more SNPs that are functionally and/or spatially linked. It is possible to combine SNPs that are disclosed in the present invention either with each other or with additional polymorphic regions to form a haplotype. Haplotypes are expected to give better predictive/diagnostic information than a single SNP.

25 In a preferred embodiment of the present invention a panel of SNPs/haplotypes is defined that predicts the risk for CVD or drug response. This predictive panel is then used for genotyping of patients on a platform that can genotype multiple SNPs at the same time (Multiplexing). Preferred platforms are e.g. gene chips (Affymetrix) or the
30 Luminex LabMAP reader. The subsequent identification and evaluation of a patient's haplotype can then help to guide specific and individualized therapy.

For example the present invention can identify patients exhibiting genetic polymorphisms or haplotypes which indicate an increased risk for adverse drug reactions. In that case the drug dose should be lowered in a way that the risk for ADR is diminished. Also if the patient's response to drug administration is particularly high (or the patient is badly metabolizing the drug), the drug dose should be lowered to avoid the risk of ADR.

In turn if the patient's response to drug administration is low (or the patient is a particularly high metabolizer of the drug), and there is no evident risk of ADR, the drug dose should be raised to an efficacious level.

It is self evident that the ability to predict a patient's individual drug response should affect the formulation of a drug, i.e. drug formulations should be tailored in a way that they suit the different patient classes (low/high responder, poor/good metabolizer, ADR prone patients). Those different drug formulations may encompass different doses of the drug, i.e. the medicinal products contains low or high amounts of the active substance. In another embodiment of the invention the drug formulation may contain additional substances that facilitate the beneficial effects and/or diminish the risk for ADR (Folkers et al. 1991, US Pat. 5,316,765).

Isolated Polymorphic Nucleic Acids, Probes, and Vectors

The present invention provides isolated nucleic acids comprising the polymorphic positions described herein for human genes; vectors comprising the nucleic acids; and transformed host cells comprising the vectors. The invention also provides probes which are useful for detecting these polymorphisms.

In practicing the present invention, many conventional techniques in molecular biology, microbiology, and recombinant DNA, are used. Such techniques are well known and are explained fully in, for example, Sambrook et al., 1989, Molecular

Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; DNA Cloning: A Practical Approach, Volumes I and II, 1985 (D. N. Glover ed.); Oligonucleotide Synthesis, 1984, (M. L. Gait ed.); Nucleic Acid Hybridization, 1985, (Hames and Higgins); Ausubel et al.,
5 Current Protocols in Molecular Biology, 1997, (John Wiley and Sons); and Methods in Enzymology Vol. 154 and Vol. 155 (Wu and Grossman, and Wu, eds., respectively).

10 Insertion of nucleic acids (typically DNAs) comprising the sequences in a functional surrounding like full length cDNA of the present invention into a vector is easily accomplished when the termini of both the DNAs and the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve
15 the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligo-
20 nucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki et al., 1988, Science 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

25 The nucleic acids may be isolated directly from cells or may be chemically synthesized using known methods. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can
30 further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by native gene sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'-
5 noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, morpholines etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by
10 formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and
15 the like.

The invention also provides nucleic acid vectors comprising the gene sequences or derivatives or fragments thereof of genes described in the Examples. A large number of vectors, including plasmid and fungal vectors, have been described for replication
25 and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for gene therapy as well as for simple cloning or protein expression. Non-limiting examples of suitable vectors include without limitation pUC plasmids, pET plasmids (Novagen, Inc., Madison, Wis.), or pRSET or pREP (Invitrogen, San Diego, Calif.), and many appropriate host cells, using methods disclosed or cited herein or otherwise
30 known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Suitable host cells may be transformed/transfected/infected as appropriate by any suitable method including electroporation, CaCl_2 mediated DNA uptake, fungal or viral infection, microinjection, microprojectile, or other established methods.

5 Appropriate host cells included bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc.

10 are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced peptides and polypeptides encoded by genes of the Examples. Nucleic acids encoding peptides or polypeptides from gene sequences of the Examples may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell and thereby effect

15 homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods such as non-homologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

20 In case of proteins that form heterodimers or other multimers, both or all subunits have to be expressed in one system or cell.

The nucleic acids of the present invention find use as probes for the detection of genetic polymorphisms and as templates for the recombinant production of normal or

25 variant peptides or polypeptides encoded by genes listed in the Examples.

Probes in accordance with the present invention comprise without limitation isolated nucleic acids of about 10-100 bp, preferably 15-75 bp and most preferably 17-25 bp in length, which hybridize at high stringency to one or more of the polymorphic

30 sequences disclosed herein or to a sequence immediately adjacent to a polymorphic position. Furthermore, in some embodiments a full-length gene sequence may be

used as a probe. In one series of embodiments, the probes span the polymorphic positions in genes disclosed herein. In another series of embodiments, the probes correspond to sequences immediately adjacent to the polymorphic positions.

5 Polymorphic Polypeptides and Polymorphism-Specific Antibodies

The present invention encompasses isolated peptides and polypeptides encoded by genes listed in the Examples comprising polymorphic positions disclosed herein. In one preferred embodiment, the peptides and polypeptides are useful screening targets
10 to identify cardiovascular drugs. In another preferred embodiment, the peptides and polypeptides are capable of eliciting antibodies in a suitable host animal that react specifically with a polypeptide comprising the polymorphic position and distinguish it from other polypeptides having a different sequence at that position.

15 Polypeptides according to the invention are preferably at least five or more residues in length, preferably at least fifteen residues. Methods for obtaining these polypeptides are described below. Many conventional techniques in protein biochemistry and immunology are used. Such techniques are well known and are explained in Immunochemical Methods in Cell and Molecular Biology, 1987 (Mayer
20 and Waler, eds; Academic Press, London); Scopes, 1987, Protein Purification: Principles and Practice, Second Edition (Springer-Verlag, N.Y.) and Handbook of Experimental Immunology, 1986, Volumes I-IV (Weir and Blackwell eds.).

25 Nucleic acids comprising protein-coding sequences can be used to direct the ITT recombinant expression of polypeptides encoded by genes disclosed herein in intact cells or in cell-free translation systems. The known genetic code, tailored if desired for more efficient expression in a given host organism, can be used to synthesize oligonucleotides encoding the desired amino acid sequences. The polypeptides may be isolated from human cells, or from heterologous organisms or cells (including, but
30 not limited to, bacteria, fungi, insect, plant, and mammalian cells) into which an

appropriate protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

5 Peptides and polypeptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, J. Am. Chem. Soc. 85:2149.

10 Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the protein contains an additional
15 sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against peptides encoded by genes disclosed herein, can be used as purification reagents. Other purification methods are possible.

20 The present invention also encompasses derivatives and homologues of the polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more
25 amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

30 The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with

a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

5 The present invention also encompasses antibodies that specifically recognize the polymorphic positions of the invention and distinguish a peptide or polypeptide containing a particular polymorphism from one that contains a different sequence at that position. Such polymorphic position-specific antibodies according to the present invention include polyclonal and monoclonal antibodies. The antibodies may be elicited in an animal host by immunization with peptides encoded by genes disclosed
10 herein or may be formed by in vitro immunization of immune cells. The immunogenic components used to elicit the antibodies may be isolated from human cells or produced in recombinant systems. The antibodies may also be produced in recombinant systems programmed with appropriate antibody-encoding DNA. Alternatively, the antibodies may be constructed by biochemical reconstitution of
15 purified heavy and light chains. The antibodies include hybrid antibodies (i.e., containing two sets of heavy chain/light chain combinations, each of which recognizes a different antigen), chimeric antibodies (i.e., in which either the heavy chains, light chains, or both, are fusion proteins), and univalent antibodies (i.e., comprised of a heavy chain/light chain complex bound to the constant region of a
20 second heavy chain). Also included are Fab fragments, including Fab' and F(ab).sub.2 fragments of antibodies. Methods for the production of all of the above types of antibodies and derivatives are well-known in the art and are discussed in more detail below. For example, techniques for producing and processing polyclonal antisera are disclosed in Mayer and Walker, 1987, Immunochemical Methods in Cell
25 and Molecular Biology, (Academic Press, London). The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., Schreier et al., 1980, Hybridoma Techniques; U.S. Pat.
30 Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against peptides encoded

by genes disclosed herein can be screened for various properties; i.e. for isotype, epitope affinity, etc.

5 The antibodies of this invention can be purified by standard methods, including but not limited to preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. Purification methods for antibodies are disclosed, e.g., in The Art of Antibody Purification, 1989, Amicon Division, W. R. Grace & Co. General protein purification methods are described in Protein Purification: Principles
10 and Practice, R. K. Scopes, Ed., 1987, Springer-Verlag, New York, N.Y.

Methods for determining the immunogenic capability of the disclosed sequences and the characteristics of the resulting sequence-specific antibodies and immune cells are well-known in the art. For example, antibodies elicited in response to a peptide
15 comprising a particular polymorphic sequence can be tested for their ability to specifically recognize that polymorphic sequence, i.e., to bind differentially to a peptide or polypeptide comprising the polymorphic sequence and thus distinguish it from a similar peptide or polypeptide containing a different sequence at the same position.

20

Kits

As set forth herein, the invention provides diagnostic methods, e.g., for determining the identity of the allelic variants of polymorphic regions present in the gene loci of
25 genes disclosed herein, wherein specific allelic variants of the polymorphic region are associated with cardiovascular diseases. In a preferred embodiment, the diagnostic kit can be used to determine whether a subject is at risk of developing a cardiovascular disease. This information could then be used, e.g., to optimize treatment of such individuals.

30

In preferred embodiments, the kit comprises a probe or primer which is capable of hybridizing to a gene and thereby identifying whether the gene contains an allelic variant of a polymorphic region which is associated with a risk for cardiovascular disease. The kit preferably further comprises instructions for use in diagnosing a subject as having, or having a predisposition, towards developing a cardiovascular disease. The probe or primers of the kit can be any of the probes or primers described in this file.

Preferred kits for amplifying a region of a gene comprising a polymorphic region of interest comprise one, two or more primers.

Antibody-based diagnostic methods and kits:

The invention also provides antibody-based methods for detecting polymorphic patterns in a biological sample. The methods comprise the steps of: (i) contacting a sample with one or more antibody preparations, wherein each of the antibody preparations is specific for a particular polymorphic form of the proteins encoded by genes disclosed herein, under conditions in which a stable antigen-antibody complex can form between the antibody and antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i) using any suitable means known in the art, wherein the detection of a complex indicates the presence of the particular polymorphic form in the sample.

Typically, immunoassays use either a labelled antibody or a labelled antigenic component (e.g., that competes with the antigen in the sample for binding to the antibody). Suitable labels include without limitation enzyme-based, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays that amplify the signals from the probe are also known, such as, for example, those that utilize biotin and avidin, and enzyme-labelled immunoassays, such as ELISA assays.

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The present invention also provides kits suitable for antibody-based diagnostic applications. Diagnostic kits typically include one or more of the following components:

- 5 (i) Polymorphism-specific antibodies. The antibodies may be pre-labelled; alternatively, the antibody may be unlabelled and the ingredients for labelling may be included in the kit in separate containers, or a secondary, labelled antibody is provided; and
- 10 (ii) Reaction components: The kit may also contain other suitably packaged reagents and materials needed for the particular immunoassay protocol, including solid-phase matrices, if applicable, and standards.

The kits referred to above may include instructions for conducting the test.

15 Furthermore, in preferred embodiments, the diagnostic kits are adaptable to high-throughput and/or automated operation.

Drug Targets and Screening Methods

20 According to the present invention, nucleotide sequences derived from genes disclosed herein and peptide sequences encoded by genes disclosed herein, particularly those that contain one or more polymorphic sequences, comprise useful targets to identify cardiovascular drugs, i.e., compounds that are effective in treating one or more clinical symptoms of cardiovascular disease. Furthermore, especially

25 when a protein is a multimeric protein that are build of two or more subunits, is a combination of different polymorphic subunits very useful.

Drug targets include without limitation (i) isolated nucleic acids derived from the genes disclosed herein, and (ii) isolated peptides and polypeptides encoded by genes

30 disclosed herein, each of which comprises one or more polymorphic positions.

In vitro screening methods:

In one series of embodiments, an isolated nucleic acid comprising one or more polymorphic positions is tested in vitro for its ability to bind test compounds in a sequence-specific manner. The methods comprise:

- (i) providing a first nucleic acid containing a particular sequence at a polymorphic position and a second nucleic acid whose sequence is identical to that of the first nucleic acid except for a different sequence at the same polymorphic position;
- (ii) contacting the nucleic acids with a multiplicity of test compounds under conditions appropriate for binding; and
- (iii) identifying those compounds that bind selectively to either the first or second nucleic acid sequence.

Selective binding as used herein refers to any measurable difference in any parameter of binding, such as, e.g., binding affinity, binding capacity, etc.

20

In another series of embodiments, an isolated peptide or polypeptide comprising one or more polymorphic positions is tested in vitro for its ability to bind test compounds in a sequence-specific manner. The screening methods involve:

- (i) providing a first peptide or polypeptide containing a particular sequence at a polymorphic position and a second peptide or polypeptide whose sequence is identical to the first peptide or polypeptide except for a different sequence at the same polymorphic position;
- (ii) contacting the polypeptides with a multiplicity of test compounds under conditions appropriate for binding; and

(iii) identifying those compounds that bind selectively to one of the nucleic acid sequences.

5 In preferred embodiments, high-throughput screening protocols are used to survey a large number of test compounds for their ability to bind the genes or peptides disclosed above in a sequence-specific manner.

Test compounds are screened from large libraries of synthetic or natural compounds.
10 Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid based compounds. Synthetic compound libraries are commercially available from Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, N.J.), Brandon Associates (Merrimack, N.H.), and Microsource (New Milford, Conn.). A rare chemical library is available from Aldrich
15 (Milwaukee, Wis.). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g. Pan Laboratories (Bothell, Wash.) or MycoSearch (N.C.), or are readily producible. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

20

In vivo screening methods

Intact cells or whole animals expressing polymorphic variants of genes disclosed herein can be used in screening methods to identify candidate cardiovascular drugs.

25

In one series of embodiments, a permanent cell line is established from an individual exhibiting a particular polymorphic pattern. Alternatively, cells (including without limitation mammalian, insect, yeast, or bacterial cells) are programmed to express a gene comprising one or more polymorphic sequences by introduction of appropriate
30 DNA. Identification of candidate compounds can be achieved using any suitable assay, including without limitation (i) assays that measure selective binding of test

compounds to particular polymorphic variants of proteins encoded by genes disclosed herein; (ii) assays that measure the ability of a test compound to modify (i.e., inhibit or enhance) a measurable activity or function of proteins encoded by genes disclosed herein; and (iii) assays that measure the ability of a compound to
5 modify (i.e., inhibit or enhance) the transcriptional activity of sequences derived from the promoter (i.e., regulatory) regions of genes disclosed herein.

In another series of embodiments, transgenic animals are created in which (i) one or more human genes disclosed herein, having different sequences at particular
10 polymorphic positions are stably inserted into the genome of the transgenic animal; and/or (ii) the endogenous genes disclosed herein are inactivated and replaced with human genes disclosed herein, having different sequences at particular polymorphic positions. See, e.g., Coffman, Semin. Nephrol. 17:404, 1997; Esther et al., Lab. Invest. 74:953, 1996; Murakami et al., Blood Press. Suppl. 2:36, 1996. Such animals
15 can be treated with candidate compounds and monitored for one or more clinical markers of cardiovascular status.

The following are intended as non-limiting examples of the invention.

20 **Material and Methods**

Genotyping of patient DNA with the PyrosequencingTM Method as described in the patent application WO 9813523:

25 First a PCR is set up to amplify the flanking regions around a SNP. Therefor 2 ng of genomic DNA (patient sample) are mixed with a primerset (20 – 40 pmol) producing a 75 to 320 bp PCR fragment with 0,3 to 1 U Qiagens Hot Star Taq PolymeraseTM in a total volume of 20 µL. One primer is biotinylated depending on the direction of the sequencing primer. To force the biotinylated primer to be incorporated it is used
30 0,8 fold.

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For primer design, programmes like Oligo 6TM (Molecular Biology Insights) or Primer SelectTM (DNASTMStar) are used. PCR setup is performed by a BioRobot 3000TM from Qiagen. PCR takes place in T1 or Tgradient ThermocyclersTM from Biometra.

- 5 The whole PCR reaction is transferred into a PSQ plateTM (Pyrosequencing) and prepared using the Sample Prep ToolTM and SNP Reagent KitTM from Pyrosequencing according to their instructions.

Preparation of template for PyrosequencingTM:

10

Sample preparation using PSQ 96 Sample Prep Tool:

1. Mount the PSQ 96 Sample Prep Tool Cover onto the PSQ 96 Sample Prep Tool as follows: Place the cover on the desk, retract the 4 attachment rods by separating the handle from the magnetic rod holder, fit the magnetic rods into
15 the holes of the cover plate, push the handle downward until a click is heard. The PSQ 96 Sample Prep Tool is now ready for use.
2. To transfer beads from one plate to another, place the covered tool into the PSQ 96 Plate containing the samples and lower the magnetic rods by separating the handle from the magnetic rod holder. Move the tool up and down a few times then wait for 30-60 seconds. Transfer the beads into a new PSQ 96 plate containing the solution of choice.
- 20 3. Release the beads by lifting the magnetic rod holder, bringing it together with the handle. Move the tool up and down a few times to make sure that the beads are released.
- 25 3. Release the beads by lifting the magnetic rod holder, bringing it together with the handle. Move the tool up and down a few times to make sure that the beads are released.

All steps are performed at room temperature unless otherwise stated.

30

Immobilization of PCR product:

Biotinylated PCR products are immobilized on streptavidin-coated Dynabeads™ M-280 Streptavidin. Parallel immobilization of several samples are performed in the
5 PSQ 96 Plate.

1. Mix PCR product, 20 µl of a well optimized PCR, with 25 µl 2X BW-buffer II. Add 60-150 µg Dynabeads. It is also possible to add a mix of Dynabeads and 2X BW-buffer II to the PCR product yielding a final BW-buffer II
10 concentration of approximately 1x.

2. Incubate at 65°C for 15 min agitation constantly to keep the beads dispersed. For optimal immobilization of fragments longer than 300 bp use 30 min incubation time.
15

Strand separation:

4. For strand separation, use the PSQ 96 Sample Prep Tool to transfer the beads with the immobilized sample to a PSQ 96 Plate containing 50 µl 0.50 M NaOH per well. Release the beads.
20
5. After approximately 1 min, transfer the beads with the immobilized strand to a PSQ 96 Plate containing 99 µl 1x Annealing buffer per well and mix thoroughly.
6. Transfer the beads to a PSQ 96 Plate containing 45 µl of a mix of 1x
25 Annealing buffer and 3-15 pmoles sequencing primer per well.
7. Heat at 80°C for 2 minutes in the PSQ 96 Sample Prep Thermoplate and move to room temperature.
8. After reaching room temperature, continue with the sequencing reaction.

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Sequencing reaction:

1. Choose the method to be used ("SNP Method") and enter relevant information in the PSQ 96 Instrument Control software.
- 5 2. Place the cartridge and PSQ 96 Plate in the PSQ 96 Instrument.
3. Start the run.

Genotyping using the ABI 7700/7900 instrument (TaqMan)

- 10 SNP genotyping using the TaqMan (Applied Biosystems/Perkin Elmer) was performed according to the manufacturer's instructions. The TaqMan assay is discussed by Lee et al., Nucleic Acids Research 1993, 21: 3761-3766.

Genotyping with a service contractor:

15

- Qiagen Genomics, formerly Rapigene, is a service contractor for genotyping SNPs in patient samples. Their method is based on a primer extension method where two complementary primers are designed for each genotype that are labeled with different tags. Depending on the genotype only one primer will be elongated together with a
- 20 certain tag. This tag can be detected with mass spectrometry and is a measure for the respective genotype. The method is described in the following patent: "Detection and identification of nucleic acid molecules - using tags which may be detected by non-fluorescent spectrometry or potentiometry" (WO 9727325).

Examples

To exemplify the present invention and its utility (the imaginary) baySNP 28 will be used in the following:

5

The nucleotide polymorphism found for baySNP 28 (e.g. C to T exchange) and the gene in which it presumably resides can be read from table 3. baySNP 28 was genotyped in various patient cohorts using primers as described in table 2. As a result the following number of patients carrying different genotypes were found (information combined from tables 3 and 5a):

10

baySNP	Cohort	Total	Genotype 11 "CC"	Genotype 12 "CT"	Genotype 22 "TT"
28	HELD_FEM_HIRES	12	1	2	9
28	HELD_FEM_LORES	22	3	12	7

When comparing the number of female patients exhibiting a high response to statin therapy (HELD_FEM_HIRES) with the control cohort (HELD_FEM_LORES) it appears that the number of low responders carrying the CT genotype is increased. This points to a lower statin response among female individuals with the CT genotype. Applying statistical tests on those findings the following p-values were obtained (data taken from table 5b):

15

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL
28	HELD_FEM_EFF	0,0506	0,0508	0,0442

20

As at least one of the GTYPE p values is below 0,05 the association of genotype and statin response phenotype is regarded as statistically significant. I.e. the analysis of a patient's genotype can predict the response to statin therapy. In more detail one can

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calculate the relative risk to exhibit a certain statin response phenotype when carrying a certain genotype (data taken from table 6a):

BAYSNP	COMPARISON	GTYPE1	GTYPE2	GTYPE3	RR1	RR2	RR3
28	HELD_FEM_EFF	CC	CT	TT	0,68	0,29	3,38

- 5 In case of baySNP 28 the risk to exhibit a high responder phenotype is 3,38 times higher when carrying the TT genotype. This indicates that a TT polymorphism in baySNP 28 is an independent risk factor for high statin response in females. On the other hand carriers of a CT or CC genotype have a reduced risk of being a high responder.

10

In addition statistical associations can be calculated on the basis on alleles. This calculation would identify risk alleles instead of risk genotypes.

In case of baySNP 28 the following allele counts were obtained (data combined from tables 3 and 5a):

15

baySNP	Cohort	Total	Allele 1 "C"	Allele 2 "T"
28	HELD_FEM_HIRES	12	4	20
28	HELD_FEM_LORES	22	18	26

- 20 When comparing the number of female patients with high statin response (HELD_FEM_HIRES) with the control cohort (HELD_FEM_LORES) it appears that the number of high responders carrying the T allele is increased, whereas the number of high responders carrying the C allele is diminished. This points to a higher statin response among female individuals with the T allele. Applying statistical tests on those findings the following p-values were obtained (data taken from table 5b):

- 52 -

BAYSNP	COMPARISON	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
28	HELD_FEM_EFF	0,0411	0,0579	0,0349

As at least one of the ALLELE p values is below 0,05 the association of allele and statin response phenotype is regarded as statistically significant (in this example significant p values were obtained from two statistical tests). I.e. also the analysis of a patient's alleles from baySNP 28 can predict the extend of statin response. In more detail one can calculate the relative risk to exhibit a certain statin response phenotype when carrying a certain allele (data taken from table 6b):

baySNP	Allele 1	Allele 2	COMPARISON	RR1	RR2
28	C	T	HELD_FEM_EFF	0,42	2,39

In case of baySNP 28 the risk to exhibit a high responder phenotype is 2,39 times higher when carrying the T allele. This indicates that the T allele of baySNP28 is an independent risk factor for a high statin response in females. In other words those patients should receive lower doses of statins in order to avoid ADR. However due to their 'high responder' phenotype they will still benefit from the drug. In turn carriers of the C allele should receive higher drug doses in order to experience a beneficial therapeutic effect.

Another example is (the imaginary) baySNP 29, which is taken to exemplify polymorphisms relevant for adverse drug reactions. baySNP 29 was found significant when comparing male patients with severe ADR to the respective controls (as defined in table 1b).

The relative risk ratios for the genotypes AA, AG and GG were as follows (data taken from table 6a):

BAYSNP	COMPARISON	GTYPE1	GTYPE2	GTYPE3	RR1	RR2	RR3
29	HBLD_MAL_ADR5ULN	AA	AG	GG	3,15	0,66	0,32

In this case male patients carrying the AA genotype have a 3,15 times higher risk to suffer from ADR. In other words those patients should either receive lower doses of statins or switch to an alternative therapy in order to avoid ADR. On the other hand
5 male patients with AG or GG genotypes appear to be more resistant to ADR and hence better tolerate statin therapy.

As can be seen from the following tables some of the associations that are disclosed in the present invention are indicative for more than one phenotype. Some baySNPs
10 can for example be linked to ADR, but also to the risk to suffer from CVD (table 6).

Sequences

The sequence section contains all phenotype associated ('PA') SNPs and adjacent
15 genomic sequences. The position of the polymorphisms that were used for the association studies ('baySNP') is indicated. Sometimes additional variations are found in the surrounding genomic sequence, that are marked by it's respective IUPAC code. Although those surrounding SNPs were not explicitly analyzed, they likely exhibit a similar association to a phenotype as the baySNP (due to linkage
20 disequilibrium, Reich D.E. et al. Nature 411, 199-204, 2001).

Table 1a Definition of "good" and "bad" serum lipid levels

	"Good"	"Bad"
LDL-Cholesterol [mg/dL]	125 -150	170 - 200
Cholesterol [mg/dL]	190 - 240	265 - 315
HDL-Cholesterol [mg/dL]	60 -105	30 - 55
Triglycerides [mg/dL]	45 - 115	170 - 450

Table 1b Definition of drug response phenotypes

Low responder	Decrease of serum LDL of at least 10% and at most 50% upon administration of 0.8 mg Cerivastatin (female patients)
High responder	Decrease of serum LDL of at least 50% upon administration of 0.4 mg Cerivastatin (female patients)
Very low responder	Decrease of serum LDL of at least 10% and at most 35% upon administration of 0.8 mg Cerivastatin (female patients)
Very high responder	Decrease of serum LDL of at least 55% upon administration of 0.4 mg Cerivastatin (female patients)
Ultra low responder	Decrease of serum LDL of at least 10% and at most 25% upon administration of 0.8 mg Cerivastatin (female patients)
Ultra high responder	Decrease of serum LDL of at least 60% upon administration of 0.4 mg Cerivastatin (female patients)
Tolerant patient	No diagnosis of muscle cramps, muscle pain, muscle weakness, myalgia or myopathy AND serum CK levels below 70 mg/dl in women and below 80 mg/dl in men.
ADR patient (CK increase at least 2×ULN)	Diagnosis of muscle cramps, muscle pain, muscle weakness, myalgia or myopathy OR serum CK levels higher than 140 mg/dl in women and 160 mg/dl in men.
Advanced ADR patient [ADR3] (advanced CK increase, at least 3×ULN)*	Serum CK levels higher than 210 mg/dl in women and 240 mg/dl in men
Severe ADR patient [ADR5] (severe CK increase, at least 5×ULN)*	Serum CK levels higher than 350 mg/dl in women and 400 mg/dl in men

*: When assembling the cohorts for advanced and severe ADR we focused on the CK serum levels as those provide a more independent measure of statin related ADR.

Table 1c Definition of "high" and "low" serum HDL cholesterol levels

	Male individuals	Female individuals
,High' HDL-Cholesterol [mg/dL]	≥ 80	≥ 104
,Low' HDL-Cholesterol [mg/dL]	≤ 35	≤ 37

An informed consent was signed by the patients and control people. Blood was taken
by a physician according to medical standard procedures.

Samples were collected anonymous and labeled with a patient number.

DNA was extracted using kits from Qiagen.

Table 2 Oligonucleotide primers used for genotyping

Depending on the method used for genotyping different oligonucleotides were
utilized. The table lists the various methods and primer sets that were used for this
invention. Primers were designed using suitable programs like Primer Express™
(Applied Biosystems, Darmstadt, Germany) or Oligo™ (Molecular Biology Insights,
Inc., Cascade, CO, USA).

Method	No. of oligonucleotides	Type of oligonucleotides
Mass Spectrometry	4	2 Primers for preamplification of the genomic fragment, 2 allele specific primers with additional tag sequences for subsequent allele spec. PCR
Pyrosequencing™	3	2 Primers for preamplification of the genomic fragment (one biotinylated), 1 sequencing primer
TaqMan	4	2 Primers for amplification of the genomic fragment, 2 allele specific probes carrying different fluorochromes (VIC, FAM) and a quencher. Preferably the allele specific probes have a minor groove binder (MGB) attached (Kutyavin et al., Nucleic Acids Research 2000, 28:655-661).

Table 3 PA SNPs, SNP classes and putative PA genes

The baySNP number refers to an internal numbering of the PA SNPs. Listed are the different polymorphisms found in our association study. Also from the association study we defined SNP classes; with ADR being adverse drug reaction related, with EFF being drug efficacy related and CVD being cardiovascular disease related. ADR3 and ADR5 relate to advanced and severe ADR, whereas VEFF and UEFF relate to very high/low and ultra high/low drug efficacy (see table 1b). Also accession numbers and descriptions of those gene loci are given that are most homologous to the PA genes as listed in the sequences section (see below). Homologous genes and their accession numbers could be found by those skilled in the art in the Genbank database. The term 'SECONDARY' marks SNPs that do not reside inside the respective gene, but in it's proximity. Null: not defined.

baySNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE22	NCBI	DESCRIPTION
29	CVD	AA	AG	GG	HS162961	Human T-lymphoma invasion and metastasis inducing TIAM1 protein (TIAM1) mRNA
29	ADR3	AA	AG	GG	HS162961	Human T-lymphoma invasion and metastasis inducing TIAM1 protein (TIAM1) mRNA
52	CVD	CC	CG	GG	X69907	H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form)
57	CVD	CC	CT	TT	M34175	Human beta adaptin mRNA, complete cds.
118	CVD	CC	CT	TT	X64229	H.sapiens dek mRNA
137	ADR5	GG	AG	AA	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.
137	ADR3	GG	AG	AA	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.
179	ADR5	GG	AG	AA	NM_000191	Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA
179	ADR3	GG	AG	AA	NM_000191	Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA
179	ADR	GG	AG	AA	NM_000191	Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA

BAF SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE13	NCBI	DESCRIPTION
240	ADR3	GG	CG	CC	X51757	Human heat-shock protein HSP70B' gene
241	ADR3	GG	AG	AA	X51757	Human heat-shock protein HSP70B' gene
241	ADR5	GG	AG	AA	X51757	Human heat-shock protein HSP70B' gene
288	CVD	GG	CG	CC	X79204	H.sapiens SCA1 mRNA for ataxin
384	CVD	CC	CG	GG	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds.
533	CVD	GG	AG	AA	X82895	H.sapiens mRNA for DLG2
542	ADR	GG	AG	AA	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.
576	CVD	CC	CT	null	D10667	Homo sapiens mRNA for smooth muscle myosin heavy chain, partial cds.
608	CVD	GG	AG	AA	M94363	Human lamin B2 (LAMB2) gene and ppv1 gene sequence.
614	CVD	GG	AG	AA	J04031	Human methylenetetrahydrofolate dehydrogenase-methylenetetrahydrofolate cyclohydrolase-formyltetrahydrofolate synthetase mRNA, complete cds.
738	CVD	AA	AC	CC	L43509	Homo sapiens methionine adenosyltransferase alpha subunit gene fragment.
1056	CVD	AA	AG	GG	Q16720	CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, ISOFORMS 3A/3B (EC 3.6.1.38) (CALCIUM PUMP) (PMCA3).
1092	ADR5	GG	CG	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
1324	CVD	CC	AC	AA	AF223404	Homo sapiens WNT1 inducible signaling pathway protein 1 (WISP1) gene, promoter and partial cds.
1574	CVD	TT	CT	CC	M57965	Homo sapiens (clones lambda gMHC 1,2,3 and 4) beta-myosin heavy chain (MYH7) gene, complete cds.
1582	ADR3	TT	CT	CC	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
1657	EFF	CC	CT	TT	J02846	Human tissue factor gene, complete cds.
1722	CVD	TT	CT	CC	D73409	Homo sapiens mRNA for diacylglycerol kinase delta, complete cds.
1756	ADR5	CC	CT	TT	M64880	Human protein C inhibitor gene, complete cds.

PLAYSMP	SNP class	GT1PE11	GT1PE12	GT1PE2	NCBI	DESCRIPTION
1757	CVD	GG	AG	AA	J04046	Human calmodulin mRNA, complete cds.
1757	VEFF	GG	AG	AA	J04046	Human calmodulin mRNA, complete cds.
1757	ADR	GG	AG	AA	J04046	Human calmodulin mRNA, complete cds.
1765	CVD	AA	AG	GG	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
1767	ADR3	TT	CT	CC	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
1767	ADR5	TT	CT	CC	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
1837	ADR3	CC	CT	TT	J00098	Human apolipoprotein A-I and C-III genes, complete cds.
1837	CVD	CC	CT	TT	J00098	Human apolipoprotein A-I and C-III genes, complete cds.
1837	ADR	CC	CT	TT	J00098	Human apolipoprotein A-I and C-III genes, complete cds.
1854	CVD	AA	AG	GG	M17712	Human cardiac myosin heavy chain mRNA, 3' end.
1862	CVD	CC	CT	TT	M92357	Homo sapiens B94 protein mRNA, complete cds.
2085	CVD	GG	GT	TT	X82540	H.sapiens mRNA for activin beta-C chain
2093	CVD	CC	CT	TT	X83543	H.sapiens APXL mRNA
2109	CVD	AA	AG	GG	Y09912	H.sapiens AP-2 beta gene
2124	CVD	GG	null	TT	Z30643	H.sapiens mRNA for chloride channel (putative) 2139bp
2140	UEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2140	EFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2140	ADR	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2140	VEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2141	ADR3	GG	AG	AA	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2141	UEFF	GG	AG	AA	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2141	ADR	GG	AG	AA	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
2186	ADR5	TT	CT	CC	M64880	Human protein C inhibitor gene, complete cds.

SNP	SNP class	GTTYPE1	GTTYPE13	GTTYPE12	GTTYPE11	NCBI	DESCRIPTION
2187	ADR3	CC	CT	TT	TT	M64880	Human protein C inhibitor gene, complete cds.
2192	ADR	GG	AG	AA	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
2192	ADR3	GG	AG	AA	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
2192	ADR5	GG	AG	AA	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
2203	CVD	TT	CT	CC	CC	L36033	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds.
2217	CVD	GG	GT	TT	TT	M15395	Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA.
2281	CVD	AA	AC	CC	CC	X87872	H. sapiens mRNA for hepatocyte nuclear factor 4c
2284	CVD	GG	AG	AA	AA	AB021744	Homo sapiens XIIIa gene for coagulation factor XIII A subunit, promoter sequence.
2290	CVD	AA	AG	GG	GG	M11309	Human coagulation factor IX mRNA, complete cds.
2327	ADR	AA	AC	CC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2327	ADR5	AA	AC	CC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2327	ADR3	AA	AC	CC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2327	EFF	AA	AC	CC	CC	M63971	Human vascular endothelial growth factor gene, exon 1.
2353	CVD	AA	AG	GG	GG	AJ246000	Homo sapiens mRNA for leucocyte adhesion receptor, L-selectin
2371	CVD	AA	AC	CC	CC	Q92679	BETA-MYOSIN HEAVY CHAIN.
2376	CVD	CC	CT	null	null	M15856	Human lipoprotein lipase mRNA, complete cds.
2401	UEFF	TT	GT	GG	GG	M18082	Human plasminogen activator inhibitor 2 (PAI-2) mRNA, complete cds.
2463	CVD	TT	CT	CC	CC	AF084225	Homo sapiens cytochrome P450 2E1 (CYP2B1) mRNA, partial cds.
2755	ADR	AA	AG	GG	GG	D63807	Human mRNA for lanosterol synthase, complete cds.
2755	EFF	AA	AG	GG	GG	D63807	Human mRNA for lanosterol synthase, complete cds.
2925	VEFF	GG	AG	AA	AA	J04501	Human muscle glycogen synthase mRNA, complete cds.
2925	UEFF	GG	AG	AA	AA	J04501	Human muscle glycogen synthase mRNA, complete cds.
3043	ADR3	GG	AG	AA	AA	U49248	ABCC2: ATP-binding cassette, sub-family C (CFTR/MRP), member 2

POS	SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE22	NCBI	DESCRIPTION
3152		VEFF	TT	AT	AA	L31573	Human sulfite oxidase mRNA, complete cds.
3214		VEFF	CC	CG	GG	L39211	Homo sapiens mitochondrial carnitine palmitoyltransferase I mRNA, complete cds.
3215		ADR5	CC	CG	null	L40027	Homo sapiens glycogen synthase kinase 3 mRNA, complete cds.
3237		CVD	CC	CG	GG	L41162	Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.
3241		ADR	TT	CT	CC	L41668	Homo sapiens UDP-galactose-4-epimerase (GALE) mRNA, complete cds.
3826		ADR5	CC	AC	AA	BC006394	Homo sapiens, COX10 (yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltransferase)
3826		ADR3	CC	AC	AA	BC006394	Homo sapiens, COX10 (yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltransferase)
3842		CVD	CC	CG	null	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds.
3843		CVD	AA	AT	TT	U12595	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds.
3869		UEFF	GG	GT	TT	U17195	Homo sapiens A-kinase anchor protein (AKAP100) mRNA, complete cds.
3942		UEFF	CC	AC	AA	BC012063	Homo sapiens, Similar to retinoid X receptor, gamma, clone MGC:19909 IMAGE:4635470, mRNA, complete cds.
4018		CVD	TT	CT	CC	BC000011	Homo sapiens, mevalonate (diphospho) decarboxylase, clone MGC:1701 IMAGE:3505156, mRNA, complete cds.
4206		ADR3	AA	AT	TT	BC000006	Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
4206		ADR	AA	AT	TT	BC000006	Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
4206		ADR5	AA	AT	TT	BC000006	Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
4527		CVD	GG	AG	AA	X76228	H.sapiens mRNA for vacuolar H+ ATPase E subunit
4527		ADR3	GG	AG	AA	X76228	H.sapiens mRNA for vacuolar H+ ATPase E subunit
4527		ADR5	GG	AG	AA	X76228	H.sapiens mRNA for vacuolar H+ ATPase E subunit
4544		ADR3	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial

BAI SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE12	NCBI	DESCRIPTION
						protein, transcript variant 1, mRNA
4544	ADR	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
4545	ADR3	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
4545	ADR	GG	AG	AA	NM_000755	Homo sapiens carnitine acetyltransferase (CRAT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
4668	ADR5	CC	AC	AA	HSKINAAANP	H. sapiens mRNA for kinase A anchor protein
4669	EFF	CC	CT	TT	HSKINAAANP	H. sapiens mRNA for kinase A anchor protein
4718	CVD	GG	AG	AA	Y09862	H. sapiens mRNA for legumain
4818	CVD	GG	AG	AA	AJ276181	Homo sapiens partial ZNF202 gene for zinc finger protein homolog, exon 5
4827	ADR5	AA	AG	GG	L07033	Human hydroxymethylglutaryl-CoA lyase mRNA, complete cds.
4838	CVD	AA	AG	GG	L08246	Human myeloid cell differentiation protein (MCL1) mRNA.
4856	CVD	GG	AG	null	L11669	Human tetracycline transporter-like protein mRNA, complete cds.
4868	ADR	TT	CT	CC	U83661	Homo sapiens multidrug resistance protein 5 (MRP5) mRNA, complete cds
4868	ADR5	TT	CT	CC	U83661	Homo sapiens multidrug resistance protein 5 (MRP5) mRNA, complete cds
4887	CVD	CC	AC	AA	AC004264	Homo sapiens PAC clone RP1-102K2 from 22q12.1-qter, complete sequence.
4912	CVD	GG	AG	AA	M63971	Human vascular endothelial growth factor gene, exon 1.
4951	ADR3	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4951	ADR5	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4951	ADR	GG	AG	AA	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4952	ADR3	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
4952	ADR5	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11

BASEP	SNP class	GTYPE11	GTYPE12	GTYPE22	NCBI	DESCRIPTION
4966	CVD	GG	AG	AA	AF133298	Homo sapiens cytochrome P450 (CYP4F8) mRNA, complete cds.
4966	ADR	GG	AG	AA	AF133298	Homo sapiens cytochrome P450 (CYP4F8) mRNA, complete cds.
5019	CVD	AA	AT	TT	D00510	Homo sapiens mRNA for calphobindin II, complete cds.
5165	ADR3	CC	AC	AA	M21574	Human platelet-derived growth factor receptor alpha (PDGFR) mRNA, complete cds.
5165	ADR5	CC	AC	AA	M21574	Human platelet-derived growth factor receptor alpha (PDGFR) mRNA, complete cds.
5165	ADR	CC	AC	AA	M21574	Human platelet-derived growth factor receptor alpha (PDGFR) mRNA, complete cds.
5278	ADR5	GG	AG	AA	D87812	Human mRNA for carnitine palmitoyltransferase I, complete cds.
5287	VEFF	CC	CT	TT	J02611	Human apolipoprotein D mRNA, complete cds.
5320	CVD	AA	AG	GG	J03799	Human colon carcinoma laminin-binding protein mRNA, complete cds.
5324	VEFF	TT	CT	CC	J04046	Human calmodulin mRNA, complete cds.
5373	ADR5	GG	GT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5375	ADR5	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5376	ADR5	AA	AT	null	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5377	ADR	TT	CT	CC	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5377	ADR5	TT	CT	CC	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
5517	ADR	AA	AG	GG	AA609457	PYRUVATE DEHYDROGENASE KINASE.
5518	ADR5	GG	CG	CC	AA609457	PYRUVATE DEHYDROGENASE KINASE.
5564	CVD	GG	GT	TT	M14584	Human interleukin 6 mRNA, complete cds.
5569	ADR5	GG	AG	AA	M14745	Human bcl-2 mRNA.
5716	ADR3	GG	CG	CC	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5716	ADR5	GG	CG	CC	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the

RAY SNP	SNP class	GTTYPE11	GTTYPE12	GENE	NCBI	DESCRIPTION
						NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5717	ADRS	GG	AG	AA	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5717	CVD	GG	AG	AA	AL008637	Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta, ESTs, STS
5850	CVD	GG	AG	AA	M95724	H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
5959	CVD	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
6151	ADR	CC	AC	AA	U49245	Human geranylgeranyl transferase type II beta-subunit mRNA, complete cds.
6236	ADR	TT	CT	CC	NM_000436	Homo sapiens 3-oxoacid CoA transferase (OXCT), nuclear gene encoding mitochondrial protein, mRNA
6277	ADRS	TT	GT	GG	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
6277	ADR	TT	GT	GG	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
6277	ADR3	TT	GT	GG	NM_003477	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
6313	UEFF	CC	CT	TT	X05199	Human mRNA for plasminogen
6369	CVD	TT	CT	CC	X52011	H.sapiens MYF6 gene encoding a muscle determination factor
6374	ADR3	TT	CT	CC	X52022	H.sapiens RNA for type VI collagen alpha3 chain
6396	CVD	TT	CT	CC	X54807	Human CYP2C8 gene for cytochrome P-450, 5' flank and exon 1
6486	CVD	GG	AG	AA	X69086	H.sapiens mRNA for utrophin

RAYSNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE22	NCBI	DESCRIPTION
6520	ADR5	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6520	ADR3	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6520	ADR	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6522	ADR3	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6522	ADR	GG	AG	AA	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6524	ADR3	AA	AG	GG	X76930	H.sapiens HNF4 mRNA for hepatocyte nuclear factor 4
6596	ADR3	CC	CT	TT	X98330	H.sapiens mRNA for ryanodine receptor 2
6596	ADR5	CC	CT	TT	X98330	H.sapiens mRNA for ryanodine receptor 2
6596	ADR	CC	CT	TT	X98330	H.sapiens mRNA for ryanodine receptor 2
6734	CVD	AA	AC	CC	AC002543	Homo sapiens BAC clone CTA-300C3 from 7q31.2, complete sequence.
6743	ADR	GG	CG	CC	X00568	Human mRNA for lipoprotein apoCII
7128	ADR3	CC	CT	TT	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
7128	ADR5	CC	CT	TT	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
7128	ADR	CC	CT	TT	J05096	Human Na,K-ATPase subunit alpha 2 (ATP1A2) gene, complete cds.
7363	CVD	GG	AG	AA	M15887	Human endozepine (putative ligand of benzodiazepine receptor) mRNA, complete cds.
7409	ADR5	AA	AG	GG	M33519	Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds.
7409	ADR3	AA	AG	GG	M33519	Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds.
8138	CVD	TT	CT	CC	AC002457	Homo sapiens BAC clone CTB-60P12 from 7q21, complete sequence.
8168	CVD	CC	AC	AA	AF019742	Homo sapiens cavolin gene, promoter region and partial cds.
8210	ADR3	GG	AG	AA	AF091582	ABC11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
8210	ADR	GG	AG	AA	AF091582	ABC11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
8241	CVD	AA	AG	GG	AF165281	Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.
8249	ADR3	CC	CT	TT	AF185589	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region.

BA XSNB	SNP class	GTTYPE11	GTTYPE12	GTTYPE2	NCBI	DESCRIPTION
8249	ADR5	CC	CT	TT	AF185589	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region.
8480	CVD	CC	CG	GG	U63415	Human peroxisome proliferator activated receptor gamma 2 mRNA, complete cds.
8577	ADR3	TT	CT	CC	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8577	ADR	TT	CT	CC	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8577	ADR5	TT	CT	CC	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8578	ADR3	GG	AG	AA	M21616	Human platelet-derived growth factor (PDGF) receptor mRNA, complete cds.
8653	ADR	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
8653	ADR3	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
8653	ADR5	CC	CT	TT	L06237	Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
8816	CVD	GG	CG	CC	L36033	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds.
8931	ADR3	CC	CT	TT	M14780	Human creatine kinase M mRNA, complete cds.
8943	ADR3	AA	AC	CC	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
9243	VEFF	CC	CG	GG	AB055890	Homo sapiens c-lbc mRNA for guanine nucleotide exchange factor Lbc, complete cds.
9243	ADR5	CC	CG	GG	AB055890	Homo sapiens c-lbc mRNA for guanine nucleotide exchange factor Lbc, complete cds.
9243	VEFF	CC	CG	GG	AB055890	Homo sapiens c-lbc mRNA for guanine nucleotide exchange factor Lbc, complete cds.
9523	ADR5	GG	AG	AA	U17195	Homo sapiens A-kinase anchor protein (AKAP100) mRNA, complete cds.
9940	CVD	CC	CT	TT	X54807	Human CYP2C8 gene for cytochrome P-450, 5' flank and exon 1
10091	ADR3	TT	CT	CC	NM_005015	Homo sapiens oxidase (cytochrome c) assembly 1-like (OXA1L), mRNA
10541	VEFF	GG	CG	CC	AF066859	Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
10541	VEFF	GG	CG	CC	AF066859	Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
10600	CVD	GG	AG	AA	AF129756	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds.

RAYSNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE2	NCBI	DESCRIPTION
10745	CVD	GG	AG	AA	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
10748	CVD	TT	CT	CC	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
10749	CVD	CC	CG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
10785	CVD	TT	CT	CC	D50678	Human mRNA for apolipoprotein E receptor 2, complete cds.
10811	CVD	AA	AG	GG	D86425	Homo sapiens mRNA for osteonidogen, complete cds.
10830	CVD	GG	AG	AA	J02610	Human apolipoprotein B-100 mRNA, complete cds.
10949	VEFF	GG	CG	CC	M10065	Human apolipoprotein E (epsilon-4 allele) gene, complete cds.
10949	EFF	GG	CG	CC	M10065	Human apolipoprotein E (epsilon-4 allele) gene, complete cds.
10962	CVD	AA	AG	GG	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
10962	ADR3	AA	AG	GG	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
10966	ADR3	TT	CT	CC	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
10966	ADR5	TT	CT	CC	M18079	Human, intestinal fatty acid binding protein gene, complete cds, and an Alu repetitive element.
11000	CVD	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11000	ADR3	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11000	ADR5	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11001	CVD	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11001	ADR3	TT	CT	CC	M34424	Human acid alpha-glucosidase (GAA) mRNA, complete cds.
11020	ADR3	CC	CT	TT	M60092	Human myoadenylate deaminase (AMPD1) mRNA, complete cds.
11073	CVD	GG	CG	CC	AF070670	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds.

SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE12	DESCRIPTION
11192	ADR5	TT	AT	AA	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
11192	ADR3	TT	AT	AA	Homo sapiens Pyruvate dehydrogenase complex, lipoyl-containing component X; E3-binding protein (PDX1), mRNA
11248	ADR3	CC	CT	TT	H.sapiens gene PACAP for pituitary adenylate cyclase activating polypeptide
11248	ADR	CC	CT	TT	H.sapiens gene PACAP for pituitary adenylate cyclase activating polypeptide
11410	VEFF	GG	GT	TT	ABCC3: ATP-binding cassette, sub-family C (CFTR/MRP), member 3
11448	CVD	GG	AG	AA	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
11448	ADR	GG	AG	AA	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
11450	CVD	TT	AT	AA	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
11456	CVD	AA	AG	GG	Homo sapiens estrogen receptor beta mRNA, complete cds.
11462	CVD	GG	GT	TT	Homo sapiens estrogen receptor beta mRNA, complete cds.
11483	ADR5	TT	CT	CC	Homo sapiens interleukin 8 receptor alpha (IL8RA) gene, complete cds.
11483	ADR3	TT	CT	CC	Homo sapiens interleukin 8 receptor alpha (IL8RA) gene, complete cds.
11483	ADR	TT	CT	CC	Homo sapiens interleukin 8 receptor alpha (IL8RA) gene, complete cds.
11531	CVD	GG	AG	AA	Human mRNA for retinoic acid receptor-like protein
11536	CVD	CC	CG	GG	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferato
11537	ADR	AA	AG	GG	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome

BAI SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE22	NCBI	DESCRIPTION
						Proliferator delta
11558	CVD	AA	AC	CC	AC006312	Homo sapiens chromosome 9, clone hRPK.401.G_18, complete sequence.
11585	CVD	GG	GT	TT	AC073593	Homo sapiens 12 BAC RP11-13J12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
11594	ADR3	TT	CT	CC	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMK1) gene, partial cds.
11594	ADR	TT	CT	CC	AF026069	Homo sapiens phosphomevalonate kinase (HUMPMK1) gene, partial cds.
11614	CVD	TT	CT	CC	AF107885	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
11631	ADR5	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
11631	ADR3	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
11637	CVD	AA	AC	CC	M19154	Human transforming growth factor-beta-2 mRNA, complete cds.
11641	ADR	GG	CG	CC	U12788	Human HMG CoA synthase mRNA, partial cds.
11645	CVD	GG	AG	AA	X05839	Human transforming growth factor-beta precursor gene exon 1 and 5' flanking region (and joined CDS)
11646	CVD	CC	CT	TT	X05839	Human transforming growth factor-beta precursor gene exon 1 and 5' flanking region (and joined CDS)
11652	CVD	CC	CT	TT	AH002776	Human low density lipoprotein receptor gene
11727	ADR5	GG	AG	AA	AB043943	Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.

SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE13	Accession	DESCRIPTION
11727	ADR3	GG	AG	AA	AB043943	Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
11728	ADR5	TT	CT	CC	AB043943	Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
11914	ADR3	AA	AT	TT	AF030555	Homo sapiens acyl-CoA synthetase 4 (ACSF4) mRNA, complete cds.
11938	ADR3	TT	CT	CC	AF058921	Homo sapiens cytosolic phospholipase A2-gamma mRNA, complete cds.
11938	ADR5	TT	CT	CC	AF058921	Homo sapiens cytosolic phospholipase A2-gamma mRNA, complete cds.
11950	ADR5	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region.
11950	ADR3	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region.
11950	ADR	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region.
11951	ADR5	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region.
11951	UEFF	GG	AG	AA	AF080222	Homo sapiens thrombin-activable fibrinolysis inhibitor gene, 5'-flanking region.
12008	ADR	CC	CT	null	AF107885	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
12031	ADR3	AA	AG	GG	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12031	ADR5	AA	AG	GG	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12031	ADR	AA	AG	GG	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12032	UEFF	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12032	ADR	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12032	VEFF	TT	CT	CC	AF091582	ABCB11: ATP-binding cassette, sub-family B (MDR/TAP), member 11
12148	ADR5	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
12148	ADR	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the

BAVSNP	SNPclass	GTTYPE11	GTTYPE12	GTTYPE23	NCBI	DESCRIPTION
						alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
12148	ADR3	GG	AG	AA	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
12207	ADR5	AA	AG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
12207	ADR	AA	AG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
12207	ADR3	AA	AG	GG	D11456	Human mRNA for Xanthine dehydrogenase, complete cds.
12399	ADR5	AA	AG	GG	D86982	Human mRNA for KIAA0229 gene, partial cds.
12399	ADR3	AA	AG	GG	D86982	Human mRNA for KIAA0229 gene, partial cds.
12399	ADR	AA	AG	GG	D86982	Human mRNA for KIAA0229 gene, partial cds.
12554	ADR	AA	AT	TT	HSVDAC1X	Human voltage-dependent anion channel isoform 1 (VDAC) mRNA, complete cds.
12554	VEFF	AA	AT	TT	HSVDAC1X	Human voltage-dependent anion channel isoform 1 (VDAC) mRNA, complete cds.
12851	ADR5	TT	CT	CC	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKARIA) mRNA, complete cds.
12851	ADR	TT	CT	CC	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKARIA) mRNA, complete cds.
13025	ADR3	AA	AC	CC	M85168	Human glycogen debranching enzyme mRNA, complete cds.
13025	ADR5	AA	AC	CC	M85168	Human glycogen debranching enzyme mRNA, complete cds.
13191	CVD	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13192	ADR3	TT	CT	CC	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13192	ADR5	TT	CT	CC	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13192	ADR	TT	CT	CC	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.

IdA3 SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE13	Accession	DESCRIPTION
13193	ADR3	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13193	ADR5	GG	AG	AA	U12789	Human clone HSH1 HMG CoA synthase mRNA, partial cds.
13338	UEFF	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13338	VEFF	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13339	ADR	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13339	CVD	GG	AG	AA	U46023	Human Xq28 mRNA, complete cds.
13340	VEFF	CC	AC	AA	U46023	Human Xq28 mRNA, complete cds.
13479	UEFF	GG	AG	AA	U95626	Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.
13633	ADR3	TT	CT	CC	HSBKTS1	H.sapiens mRNA for glycerol kinase testis specific 1.
13633	ADR	TT	CT	CC	HSBKTS1	H.sapiens mRNA for glycerol kinase testis specific 1.
13929	ADR5	GG	AG	AA	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds.
14065	EFF	CC	CT	TT	AC006022	Homo sapiens PAC clone RP5-1131G17 from 7p15.1-p14, complete sequence.
14083	ADR	TT	CT	CC	AF044953	Homo sapiens NADH:ubiquinone oxidoreductase PGIV subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.
14085	EFF	TT	CT	CC	AF044954	Homo sapiens NADH:ubiquinone oxidoreductase PDSW subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.
14087	EFF	TT	CT	CC	AF044954	Homo sapiens NADH:ubiquinone oxidoreductase PDSW subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.
14102	ADR5	CC	CT	TT	AF087661	Homo sapiens NADH:ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14102	EFF	CC	CT	TT	AF087661	Homo sapiens NADH:ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.

SNP	SNP class	GTTYPE1	GTTYPE2	GTTYPE12	GTTYPE22	NCBI	DESCRIPTION
14103	EFF	CC	CT	TT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14103	VEFF	CC	CT	TT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14103	UEFF	CC	CT	TT	TT	AF087661	Homo sapiens NADH-ubiquinone oxidoreductase 42 kDa subunit mRNA, complete cds, nuclear gene encoding mitochondrial protein.
14129	ADR3	AA	AG	GG	GG	BC003093	Homo sapiens, Rab geranylgeranyltransferase, alpha subunit, clone MGC:1485 IMAGE:3537388, mRNA, complete cds.
14326	EFF	AA	AC	CC	CC	NM_005390	Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA
14503	ADR5	CC	CT	TT	TT	AJ276178	Homo sapiens partial ZNF202 gene for zinc finger protein homolog, exon 2
14503	ADR3	CC	CT	TT	TT	AJ276178	Homo sapiens partial ZNF202 gene for zinc finger protein homolog, exon 2
14537	ADR	CC	CT	TT	TT	U22526	Human 2,3-oxidosqualene-lanosterol cyclase mRNA, complete cds.
15915	ADR	TT	CT	CC	CC	L32179	Human arylacetamide deacetylase mRNA, complete cds.
15915	ADR3	TT	CT	CC	CC	L32179	Human arylacetamide deacetylase mRNA, complete cds.
19289	CVD	GG	AG	AA	AA	AL031651	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2)
36958	ADR3	CC	CG	GG	GG	AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
37158	ADR	CC	AC	AA	AA	D63807	Human mRNA for lanosterol synthase, complete cds.
37160	UEFF	CC	CT	TT	TT	D63807	Human mRNA for lanosterol synthase, complete cds.
37412	ADR5	TT	GT	GG	GG	M74775	Human lysosomal acid lipase/cholesteryl esterase mRNA, complete cds.
37412	ADR3	TT	GT	GG	GG	M74775	Human lysosomal acid lipase/cholesteryl esterase mRNA, complete cds.
37457	CVD	TT	AT	AA	AA	S67973	NDUFV1=NADH-ubiquinone oxidoreductase flavoprotein 1 subunit [human, kidney, mRNA Partial, 771 nt].
37704	ADR5	CC	CT	null	null	XM_010049	Homo sapiens peroxisome proliferative activated receptor, alpha (PPARA), mRNA.

RAY	SNP class	GTTYPE11	GTTYPE12	GTTYPE13	GTTYPE14	DESCRIPTION
38959	CVD	CC	AC	AA	AL133392	Human DNA sequence from clone C1TF22-45C1 on chromosome 22 Contains the 3' part of the CSF2RB gene for low-affinity granulocyte-macrophage colony stimulating factor 2 receptor beta, the CSF2RB2 gene for colony stimulating factor 2 receptor beta 2, ESTs, STS
38959	EFF	CC	AC	AA	AL133392	Human DNA sequence from clone C1TF22-45C1 on chromosome 22 Contains the 3' part of the CSF2RB gene for low-affinity granulocyte-macrophage colony stimulating factor 2 receptor beta, the CSF2RB2 gene for colony stimulating factor 2 receptor beta 2, ESTs, STS
39292	ADR5	GG	AG	AA	M33388	Human cytochrome P450 IID6 (CYP2D6) gene, complete cds.
39698	ADR3	TT	CT	CC	X07619	Human mRNA for cytochrome P450 db1 variant b
39756	ADR3	TT	CT	CC	X58468	Human CYP2D7BP pseudogene for cytochrome P450 2D6
39951	ADR	TT	CT	CC	AF005896	Homo sapiens Na K-ATPase beta-3 subunit (atp1b3) gene, exon 7 and complete cds.
39951	ADR5	TT	CT	CC	AF005896	Homo sapiens Na K-ATPase beta-3 subunit (atp1b3) gene, exon 7 and complete cds.
40466	EFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
40466	UEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
40466	VEFF	GG	GT	TT	AB043821	Homo sapiens GPVI mRNA for platelet glycoprotein VI-3, complete cds.
44442	ADR5	AA	AG	GG	NM_001931	Homo sapiens dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) (DLAT), mRNA
55504	ADR	TT	CT	CC	SECONDARY: NM_000191	SECONDARY TO Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA
55542	ADR	CC	AC	AA	SECONDARY: NM_000191	SECONDARY TO Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria) (HMGCL), mRNA
55670	VEFF	CC	CT	TT	SECONDARY: NM_001876	SECONDARY TO Homo sapiens carnitine palmitoyltransferase I, liver (CPT1A), nuclear gene encoding mitochondrial protein, mRNA
55736	ADR5	AA	AG	GG	SECONDARY: M23234	SECONDARY TO ABCB4

RAISNP	SNP class	GTTYPE1	GTTYPE2	GTTYPE12	NCBI	DESCRIPTION
55748	ADR5	TT	CT	CC	SECONDARY: M23234	SECONDARY TO ABCB4
55813	ADR3	TT	CT	CC	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55845	VEFF	CC	AC	AA	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55845	ADR3	CC	AC	AA	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55845	UEFF	CC	AC	AA	SECONDARY: M34551	SECONDARY TO Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.
55923	ADR	CC	CT	TT	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
55923	ADR3	CC	CT	TT	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
55945	ADR	GG	AG	AA	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
55945	ADR3	GG	AG	AA	SECONDARY: M95724	SECONDARY TO H.sapiens centromere autoantigen C (CENPC) mRNA, complete cds.
56007	ADR3	TT	CT	CC	SECONDARY: NM_001303	SECONDARY TO Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA
56007	ADR5	TT	CT	CC	SECONDARY: NM_001303	SECONDARY TO Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA

BAVSNP	SNP class	GTTYPE1	GTTYPE2	GTTYPE3	NCBI	DESCRIPTION
56011	ADR5	AA	AG	null	SECONDARY: NM_001303	SECONDARY TO Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA
56104	UEFF	GG	AG	AA	SECONDARY: AF091582	SECONDARY TO ABCB11
56113	ADR5	GG	GT	TT	SECONDARY: AF091582	SECONDARY TO ABCB11
56113	ADR3	GG	GT	TT	SECONDARY: AF091582	SECONDARY TO ABCB11
56636	ADR	TT	CT	CC	SECONDARY: L13972	SECONDARY TO Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds.
56636	ADR3	TT	CT	CC	SECONDARY: L13972	SECONDARY TO Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds.
56636	ADR5	TT	CT	CC	SECONDARY: L13972	SECONDARY TO Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds.
56666	ADR3	GG	AG	AA	SECONDARY: AF027406	SECONDARY TO Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56666	ADR5	GG	AG	AA	SECONDARY: AF027406	SECONDARY TO Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56666	ADR	GG	AG	AA	SECONDARY: AF027406	SECONDARY TO Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56667	EFF	TT	CT	CC	AF027406	Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56667	ADR3	TT	CT	CC	AF027406	Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA, complete cds.
56780	ADR3	GG	AG	AA	SECONDARY:	SECONDARY TO Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide

BAISNP	SNP class	GTTYPE1	GTTYPE2	GTTYPE3	CHROM	NCBI	DESCRIPTION
						BC000006	
56780	ADR	GG	AG	AA		SECONDARY: BC000006	SECONDARY TO Homo sapiens, ATPase, Na+/K+ transporting, beta 1 polypeptide
56876	UEFF	TT	CT	CC		SECONDARY: AF066859	SECONDARY TO Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
56876	EFF	TT	CT	CC		SECONDARY: AF066859	SECONDARY TO Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
56876	VEFF	TT	CT	CC		SECONDARY: AF066859	SECONDARY TO Homo sapiens muscle glycogen phosphorylase (PYGM) mRNA, complete cds.
56978	ADR5	AA	AG	GG		SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57000	VEFF	AA	AT	TT		SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57000	UEFF	AA	AT	TT		SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57000	CVD	AA	AT	TT		SECONDARY: D11456	SECONDARY TO Human mRNA for Xanthine dehydrogenase, complete cds.
57313	UEFF	TT	CT	CC		SECONDARY: AB014460	SECONDARY TO Homo sapiens TSC2, NTHL1/NTH1 and SLC9A3R2/E3KARP genes, partial and complete cds.
57734	ADR3	CC	CG	GG		SECONDARY: AL022721	SECONDARY TO Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator delta
57837	ADR3	AA	AG	GG		SECONDARY:	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.

BASENP	SNP class	GTTYPE1	GTTYPE2	GTTYPE3	DESCRIPTION
				AB043943	
57853	BFF	TT	CT	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57853	UEFF	TT	CT	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57853	VEFF	TT	CT	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57854	EFF	GG	AG	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57854	UEFF	GG	AG	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
57854	ADR3	GG	AG	SECONDARY: AB043943	SECONDARY TO Homo sapiens GPVI gene for platelet glycoprotein VI, partial cds.
58295	ADR	AA	AG	SECONDARY: X83618	SECONDARY TO H.sapiens mRNA for 3-hydroxy-3-methylglutaryl coenzyme A synthase
58402	ADR3	TT	CT	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58407	VEFF	GG	GT	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA; complete cds.
58407	UEFF	GG	GT	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58440	UEFF	TT	CT	SECONDARY: U46023	SECONDARY TO Human Xq28 mRNA, complete cds.
58525	ADR	CC	CT	SECONDARY: TT	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA

RAYSNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE22	NCBI	DESCRIPTION
					NM_013240	
58525	ADR3	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58525	ADR5	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58533	ADR	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58533	ADR3	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58533	ADR5	CC	CT	TT	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58544	ADR5	GG	AG	AA	SECONDARY: NM_013240	SECONDARY TO Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
58716	ADR3	TT	CT	CC	SECONDARY: BC002772	SECONDARY TO Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14), clone MGC:3686 IMAGE:3619356, mRNA, complete cds.
58716	ADR5	TT	CT	CC	SECONDARY: BC002772	SECONDARY TO Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14), clone MGC:3686 IMAGE:3619356, mRNA, complete cds.
58736	EFF	CC	CT	TT	SECONDARY: BC002772	SECONDARY TO Homo sapiens, NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14kD, B14), clone MGC:3686 IMAGE:3619356, mRNA, complete cds.
58808	ADR	AA	AG	GG	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2
58809	ADR5	CC	AC	AA	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2
58809	ADR3	CC	AC	AA	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2

SNP	SNP class	GTTYPE1	GTTYPE2	GENOTYPE	NCH	DESCRIPTION
					NM_003889	
58809	UEFF	CC	AC	AA	SECONDARY: NM_003889	SECONDARY TO nuclear hormone receptor PRR2
58886	ADR3	AA	AG	GG	SECONDARY: AL008637	SECONDARY TO Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta
58886	ADR5	AA	AG	GG	SECONDARY: AL008637	SECONDARY TO Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2 Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD), the 5' part of the CSF2RB gene for granulocyte-macrophage low-affinity colony stimulating factor 2 receptor beta
58926	ADR3	CC	CT	TT	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58926	ADR5	CC	CT	TT	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58926	CVD	CC	CT	TT	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58968	ADR5	AA	AG	GG	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58968	ADR3	AA	AG	GG	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
58985	ADR5	GG	AG	AA	SECONDARY: L78810	SECONDARY TO Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.
59113	ADR5	CC	CG	GG	SECONDARY: L78810	SECONDARY TO Homo sapiens acyl-CoA synthetase 4 (ACSA4) mRNA, complete cds.

SNP	SNP class	GTTYPE1	GTTYPE2	GTTYPE2	NCBI	DESCRIPTION
59113	ADR3	CC	CG	GG	SECONDARY: AF030555	SECONDARY TO Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds.
59236	ADR	GG	AG	AA	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59236	ADR3	GG	AG	AA	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59237	VEFF	CC	CT	TT	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59237	BFF	CC	CT	TT	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59267	UEFF	TT	CT	CC	SECONDARY: NM_002340	SECONDARY TO Homo sapiens lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), mRNA
59352	ADR	TT	CT	CC	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59363	CVD	TT	CT	CC	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59368	ADR	TT	CT	CC	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59371	VEFF	CC	CT	TT	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59371	UEFF	CC	CT	TT	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59372	ADR	CC	CT	TT	SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.

BAFSNP	SNP class	GT/PE11	GT/PE12	GT/PE13	GT/PE14	GT/PE15	DESCRIPTION
						M34960	
59372	ADR3	CC	CT	TT		SECONDARY: M34960	SECONDARY TO Homo sapiens transcription factor IID mRNA, complete cds.
59443	ADR5	TT	CT	CC		SECONDARY: U84007	SECONDARY TO Human glycogen debranching enzyme isoform 1 (AGL) mRNA, alternatively spliced isoform, complete cds.
900080	ADR3	GG	CG	CC		NM_013240	Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
900080	ADR5	GG	CG	CC		NM_013240	Homo sapiens putative N6-DNA-methyltransferase (N6AMT1), mRNA
900102	UEFF	TT	GT	GG		NM_003889	nuclear hormone receptor PRR2
900102	VEFF	TT	GT	GG		NM_003889	nuclear hormone receptor PRR2
900111	UEFF	GG	AG	AA		NM_003889	nuclear hormone receptor PRR2
900111	VEFF	GG	AG	AA		NM_003889	nuclear hormone receptor PRR2
900117	CVD	TT	GT	GG		AF050163	Homo sapiens lipoprotein lipase precursor, gene, partial cds.
900118	EFF	GG	AG	AA		U46024	MTM1: myotubular myopathy 1
900118	VEFF	GG	AG	AA		U46024	MTM1: myotubular myopathy 1
900118	ADR5	GG	AG	AA		U46024	MTM1: myotubular myopathy 1
900120	EFF	TT	CT	CC		U46024	MTM1: myotubular myopathy 1
900121	EFF	TT	GT	GG		U58033	MTMR2: myotubularin related protein 2
900123	ADR	AA	AG	ml		U58033	MTMR2: myotubularin related protein 2
900124	EFF	GG	AG	AA		U58033	MTMR2: myotubularin related protein 2
900132	ADR	TT	CT	CC		AF169257	SLC24A3: solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
900144	CVD	AA	AG	GG		AC008945	Selenoprotein P genomic region
900144	ADR5	AA	AG	GG		AC008945	Selenoprotein P genomic region
900145	CVD	GG	GT	TT		AC008945	Selenoprotein P genomic region

BAVSNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE13	SNCH	DEFINITION
900145	ADR5	GG	GT	TT	AC008945	Selenoprotein P genomic region
900146	ADR5	AA	AG	GG	AC008945	Selenoprotein P genomic region
900146	CVD	AA	AG	GG	AC008945	Selenoprotein P genomic region
900146	ADR	AA	AG	GG	AC008945	Selenoprotein P genomic region
900147	ADR3	TT	CT	CC	AC008945	Selenoprotein P genomic region
900196	CVD	CC	CT	TT	G62788	SHGC-140326 Human Homo sapiens STS genomic, sequence tagged site.
900196	ADR3	CC	CT	TT	G62788	SHGC-140326 Human Homo sapiens STS genomic, sequence tagged site.
900200	CVD	TT	CT	CC	AF101918	Human Homo sapiens genomic clone pTWB28.01, DNA sequence.
900204	EFF	CC	CG	null	NM_016347	N-Acetyltransferase Camello 2
900205	EFF	CC	CG	GG	NM_016347	N-Acetyltransferase Camello 2
900205	CVD	CC	CG	GG	NM_016347	N-Acetyltransferase Camello 2
900223	ADR	GG	AG	AA	AK055126	HIS cDNA FLJ30564 fis
900225	ADR5	GG	AG	AA	AJ227891	Homo sapiens partial mRNA; ID ED166-4A2
900225	ADR3	GG	AG	AA	AJ227891	Homo sapiens partial mRNA; ID ED166-4A2
900227	ADR5	AA	AC	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900233	ADR5	TT	AT	AA	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900236	ADR3	CC	CT	TT	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900236	ADR5	CC	CT	TT	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900241	EFF	CC	CG	GG	SECONDARY:	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)

RAY SNP	SNP class	GTTYPE11	GTTYPE12	GTTYPE2	NCBI	DESCRIPTION
					AJ000414	
900242	ADR5	GG	CG	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900242	ADR3	GG	CG	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)
900242	ADR	GG	CG	CC	SECONDARY: AJ000414	SECONDARY TO Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4)

Table 4 Cohorts

Given are names (as used in table 5) and formations of the various cohorts that were used for genotyping

COHORT	Definition
HELD_ALL_GOOD/BAD	Healthy elderly individuals of both genders with good or bad serum lipid profiles (as defined in table 1a)
HELD_FEM_GOOD/BAD	Healthy elderly individuals (female) with good or bad serum lipid profiles (as defined in table 1a)
HELD_MAL_GOOD/BAD	Healthy elderly individuals (male) with good or bad serum lipid profiles (as defined in table 1a)
CVD_ALL_CASE/CTRL	Individuals with diagnosis of cardiovascular disease and healthy controls (both genders)
CVD_FEM_CASE/CTRL	Individuals with diagnosis of cardiovascular disease and healthy controls (female)
CVD_MAL_CASE/CTRL	Individuals with diagnosis of cardiovascular disease and healthy controls (male)
HELD_FEM_ADRCTRL	Female individuals that tolerate administration of cerivastatin without exhibiting signs of ADR (as defined in table 1b)
HELD_FEM_ADRCASE	Female individuals that exhibited ADR (as defined in table 1b) upon administration of cerivastatin
HELD_MAL_ADRCTRL	Male individuals that tolerate administration of cerivastatin without exhibiting signs of ADR (as defined in table 1b)
HELD_MAL_ADRCASE	Male individuals that exhibited ADR (as defined in table 1b) upon administration of cerivastatin
HELD_ALL_ADRCTRL	Individuals of both genders that tolerate administration of cerivastatin without exhibiting signs of ADR (as defined in table 1b)
HELD_ALL_ADRCASE	Individuals of both genders that exhibited ADR (as defined in table 1b) upon administration of cerivastatin
HELD_FEM_LORESP	Female individuals with a minor response to cerivastatin administration (as defined in table 1b)
HELD_FEM_HIRES	Female individuals with a high response to cerivastatin administration (as defined in table 1b)
HELD_FEM_HHDL/LOHDL	Healthy elderly individuals (female) with high or low serum HDL cholesterol levels (as defined in table 1c)
HELD_MAL_HHDL/LOHDL	Healthy elderly individuals (male) with high or low serum HDL cholesterol levels (as defined in table 1c)
HELD_ALL_HHDL/LOHDL	Healthy elderly individuals of both genders with high or low serum HDL cholesterol levels (as defined in table 1c)
HELD_FEM_ADR3CASE	Female individuals that exhibited advanced ADR (as defined in table 1b) upon administration of cerivastatin

COHORT	Definition
HELD_MAL_ADR3CASE	Male individuals that exhibited advanced ADR (as defined in table 1b) upon administration of cerivastatin
HELD_ALL_ADR3CASE	Individuals of both genders that exhibited advanced ADR (as defined in table 1b) upon administration of cerivastatin
HELD_FEM_VLORESP	Female individuals with a very low response to cerivastatin administration (as defined in table 1b)
HELD_FEM_VHIRESP	Female individuals with a very high response to cerivastatin administration (as defined in table 1b)
HELD_FEM_ADR5CASE	Female individuals that exhibited severe ADR (as defined in table 1b) upon administration of cerivastatin
HELD_MAL_ADR5CASE	Male individuals that exhibited severe ADR (as defined in table 1b) upon administration of cerivastatin
HELD_ALL_ADR5CASE	Individuals of both genders that exhibited severe ADR (as defined in table 1b) upon administration of cerivastatin
HELD_FEM_ULORESP	Female individuals with a ultra low response to cerivastatin administration (as defined in table 1b)
HELD_FEM_UHIRESP	Female individuals with a ultra high response to to cerivastatin administration (as defined in table 1b)

Table 5a and 5b

The baySNP number refers to an internal numbering of the PA SNPs. Cpval denotes the classical Pearson chi-squared test, Xpval denotes the exact version of Pearson's chi-squared test, LRpval denotes the likelihood-ratio chi-squared test, Cpvalue, Xpvalue, and LRpvalue are calculated as described in (SAS/STAT User's Guide of the SAS OnlineDoc, Version 8), (L. D. Fisher and G. van Belle, Biostatistics, Wiley Interscience 1993), and (A. Agresti, Statistical Science 7, 131 (1992)). The GTYPE and Allele p values were obtained through the respective chi square tests when comparing COHORTs A and B. For GTYPE p value the number of patients in cohort A carrying genotypes 11, 12 or 22 (FQ11 A, FQ 12 A, FQ 22 A; genotypes as defined in table 3) were compared with the respective patients in cohort B (FQ11 B, FQ 12 B, FQ 22 B; genotypes as defined in table 3) resulting in the respective chi square test with a 3x2 matrix. For Allele p values we compared the allele count of alleles 1 and 2 (A1 and A2) in cohorts A and B, respectively (chi square test with a 2x2 matrix). SIZE A and B: Number of patients in cohorts A and B, respectively. See table 4 for definition of COHORTs A and B.

Table 5a
Cohort sizes and frequency of alleles and genotypes

baySNP	A1/A2	COORPT_A	SIZE	FOI1_A	FOI2_A	FOI1_B	FOI2_B	COHORT_B	SIZE_B	FOI1_B	FOI2_B	FOI1_B	FOI2_B
29	A	G	80	100	60	32	36	12	78	80	76	19	42
29	A	G	47	54	40	21	12	14	131	125	137	35	55
29	A	G	99	122	76	39	44	16	114	119	109	29	61
52	C	G	43	42	44	11	20	12	39	57	21	22	13
52	C	G	18	20	16	3	14	1	25	29	21	10	9
52	C	G	29	27	31	6	15	8	22	30	14	11	8



DAYSP	AL A2	COHORT A	SIZE	FO	FO A	FOLE	FOLE	NO	COHORT B	SIZE	FO B	FO B	FO B	FO B	FO B
1757	G A	HELD_ALL_CASE	45	63	27	25	13	7	HELD_ALL_CTRL	38	58	18	20	18	0
1757	G A	HELD_FEM_CASE	31	40	22	16	8	7	HELD_FEM_CTRL	21	33	9	12	9	0
1757	G A	HELD_FEM_VHRESP	148	177	119	52	73	23	HELD_FEM_VLORESP	152	206	98	70	66	16
1757	G A	HELD_MAL_ADRCASE	62	90	34	30	30	2	HELD_MAL_ADRCTRL	58	87	29	35	17	6
1765	A G	HELD_ALL_BAD	100	29	171	6	17	77	HELD_ALL_GOOD	107	39	175	3	33	71
1767	T C	HELD_ALL_ADRCASE3ULN	40	75	5	36	3	1	HELD_ALL_ADRCTRL	107	172	42	69	34	4
1767	T C	HELD_ALL_ADRCASE5ULN	21	40	2	19	2	0	HELD_ALL_ADRCTRL	107	172	42	69	34	4
1767	T C	HELD_MAL_ADRCASE5ULN	7	0	14	7	0	0	HELD_MAL_ADRCTRL	53	86	20	35	16	2
1767	T C	HELD_FEM_ADRCASE3ULN	27	50	4	24	2	1	HELD_FEM_ADRCTRL	54	86	22	34	18	2
1767	T C	HELD_MAL_ADRCASE3ULN	13	25	1	12	1	0	HELD_MAL_ADRCTRL	53	86	20	35	16	2
1837	C T	HELD_ALL_ADRCASE3ULN	48	75	21	29	17	2	HELD_ALL_ADRCTRL	132	173	91	52	69	11
1837	C T	HELD_FEM_BAD	81	120	42	49	22	10	HELD_FEM_GOOD	79	109	49	36	37	6
1837	C T	HELD_ALL_BAD	100	145	55	58	29	13	HELD_ALL_GOOD	115	158	72	53	52	10
1837	C T	HELD_ALL_ADRCASE	134	195	73	72	51	11	HELD_ALL_ADRCTRL	132	173	91	52	69	11
1854	A G	HELD_FEM_BAD	80	85	75	21	43	16	HELD_FEM_GOOD	79	100	58	35	30	14
1862	C T	HELD_FEM_BAD	80	121	39	44	33	3	HELD_FEM_GOOD	76	97	55	29	39	8
2085	G T	HELD_FEM_CASE	31	44	18	14	16	1	HELD_FEM_CTRL	22	20	24	4	12	6
2085	G T	HELD_ALL_CASE	45	61	29	19	23	3	HELD_ALL_CTRL	40	40	40	10	20	10
2093	C T	HELD_MAL_CASE	14	15	13	7	1	6	HELD_MAL_CTRL	18	32	4	16	0	2
2093	C T	HELD_ALL_CASE	45	62	28	25	12	8	HELD_ALL_CTRL	40	66	14	28	10	2
2109	A G	HELD_MAL_LOHDL	19	34	4	16	2	1	HELD_MAL_HHDL	22	31	13	9	13	0

DAYSNP	AT1A2	COHORT_A	SIZE_A	FQ1A	FQ2_A	FQ1B	FQ12_A	FQ22_A	COHORT_B	SIZE_B	FQ1_B	FQ2_B	FQ12_B	FQ22_B	
2109	A	G	HELD_ALL_LOHDL	39	70	8	32	6	1	HELD_ALL_HIHDL	48	76	20	28	0
2109	A	G	HELD_ALL_BAD2	624	1035	213	432	171	21	HELD_ALL_GOOD2	700	1109	291	439	30
2109	A	G	HELD_FEM_BAD	80	139	21	60	19	1	HELD_FEM_GOOD	78	120	36	45	3
2124	G	T	HELD_MAL_BAD	17	14	20	7	0	10	HELD_MAL_GOOD	32	40	24	20	12
2140	G	T	HELD_FEM_UHRESP	43	79	7	36	7	0	HELD_FEM_ULORESP	60	94	26	38	4
2140	G	T	HELD_FEM_HIRES	237	416	58	181	54	2	HELD_FEM_LORESP	239	390	88	161	10
2140	G	T	HELD_MAL_ADRCASE	46	80	12	34	12	0	HELD_MAL_ADRCTRL	49	73	25	29	5
2140	G	T	HELD_FEM_VHRESP	119	207	31	90	27	2	HELD_FEM_VLORESP	122	194	50	77	5
2141	G	A	HELD_MAL_ADRCASE3ULN	16	30	2	14	2	0	HELD_MAL_ADRCTRL	52	78	26	30	4
2141	G	A	HELD_FEM_UHRESP	53	91	15	38	15	0	HELD_FEM_ULORESP	77	121	33	51	7
2141	G	A	HELD_MAL_ADRCASE	58	100	16	42	16	0	HELD_MAL_ADRCTRL	52	78	26	30	4
2186	T	C	HELD_MAL_ADRCASE3ULN	9	14	4	6	2	1	HELD_MAL_ADRCTRL	59	109	9	50	0
2187	C	T	HELD_FEM_ADRCASE3ULN	30	37	23	10	17	3	HELD_FEM_ADRCTRL	71	107	35	42	6
2192	G	A	HELD_FEM_ADRCASE	69	137	1	68	1	0	HELD_FEM_ADRCTRL	70	127	13	57	0
2192	G	A	HELD_FEM_ADRCASE3ULN	30	0	60	30	0	0	HELD_FEM_ADRCTRL	70	127	13	57	0
2192	G	A	HELD_ALL_ADRCASE	132	258	6	126	6	0	HELD_ALL_ADRCTRL	126	233	19	108	1
2192	G	A	HELD_FEM_ADRCASE3ULN	16	0	32	16	0	0	HELD_FEM_ADRCTRL	70	127	13	57	0
2192	G	A	HELD_ALL_ADRCASE3ULN	47	92	2	45	2	0	HELD_ALL_ADRCTRL	126	233	19	108	1
2203	T	C	HELD_FEM_BAD	80	106	54	32	42	6	HELD_FEM_GOOD	79	125	33	50	4
2203	T	C	HELD_ALL_BAD	98	128	68	39	50	9	HELD_ALL_GOOD	115	171	59	66	10
2217	G	T	HELD_MAL_CASE	13	14	12	2	10	1	HELD_MAL_CTRL	17	29	5	12	0

WHSNT	AL A2	COHORT_A	SIZE	FOIA	FOI1	FOI2	COHORT_B	SIZE	FOI1	FOI2	FOI3	FOI4	FOI5	FOI6	FOI7	FOI8	FOI9	FOI10	FOI11	FOI12	FOI13	FOI14	FOI15	FOI16	FOI17	FOI18	FOI19	FOI20	FOI21	FOI22	FOI23	FOI24	FOI25	FOI26	FOI27	FOI28	FOI29	FOI30	FOI31	FOI32	FOI33	FOI34	FOI35	FOI36	FOI37	FOI38	FOI39	FOI40	FOI41	FOI42	FOI43	FOI44	FOI45	FOI46	FOI47	FOI48	FOI49	FOI50	FOI51	FOI52	FOI53	FOI54	FOI55	FOI56	FOI57	FOI58	FOI59	FOI60	FOI61	FOI62	FOI63	FOI64	FOI65	FOI66	FOI67	FOI68	FOI69	FOI70	FOI71	FOI72	FOI73	FOI74	FOI75	FOI76	FOI77	FOI78	FOI79	FOI80	FOI81	FOI82	FOI83	FOI84	FOI85	FOI86	FOI87	FOI88	FOI89	FOI90	FOI91	FOI92	FOI93	FOI94	FOI95	FOI96	FOI97	FOI98	FOI99	FOI100	FOI101	FOI102	FOI103	FOI104	FOI105	FOI106	FOI107	FOI108	FOI109	FOI110	FOI111	FOI112	FOI113	FOI114	FOI115	FOI116	FOI117	FOI118	FOI119	FOI120	FOI121	FOI122	FOI123	FOI124	FOI125	FOI126	FOI127	FOI128	FOI129	FOI130	FOI131	FOI132	FOI133	FOI134	FOI135	FOI136	FOI137	FOI138	FOI139	FOI140	FOI141	FOI142	FOI143	FOI144	FOI145	FOI146	FOI147	FOI148	FOI149	FOI150	FOI151	FOI152	FOI153	FOI154	FOI155	FOI156	FOI157	FOI158	FOI159	FOI160	FOI161	FOI162	FOI163	FOI164	FOI165	FOI166	FOI167	FOI168	FOI169	FOI170	FOI171	FOI172	FOI173	FOI174	FOI175	FOI176	FOI177	FOI178	FOI179	FOI180	FOI181	FOI182	FOI183	FOI184	FOI185	FOI186	FOI187	FOI188	FOI189	FOI190	FOI191	FOI192	FOI193	FOI194	FOI195	FOI196	FOI197	FOI198	FOI199	FOI200	FOI201	FOI202	FOI203	FOI204	FOI205	FOI206	FOI207	FOI208	FOI209	FOI210	FOI211	FOI212	FOI213	FOI214	FOI215	FOI216	FOI217	FOI218	FOI219	FOI220	FOI221	FOI222	FOI223	FOI224	FOI225	FOI226	FOI227	FOI228	FOI229	FOI230	FOI231	FOI232	FOI233	FOI234	FOI235	FOI236	FOI237	FOI238	FOI239	FOI240	FOI241	FOI242	FOI243	FOI244	FOI245	FOI246	FOI247	FOI248	FOI249	FOI250	FOI251	FOI252	FOI253	FOI254	FOI255	FOI256	FOI257	FOI258	FOI259	FOI260	FOI261	FOI262	FOI263	FOI264	FOI265	FOI266	FOI267	FOI268	FOI269	FOI270	FOI271	FOI272	FOI273	FOI274	FOI275	FOI276	FOI277	FOI278	FOI279	FOI280	FOI281	FOI282	FOI283	FOI284	FOI285	FOI286	FOI287	FOI288	FOI289	FOI290	FOI291	FOI292	FOI293	FOI294	FOI295	FOI296	FOI297	FOI298	FOI299	FOI300	FOI301	FOI302	FOI303	FOI304	FOI305	FOI306	FOI307	FOI308	FOI309	FOI310	FOI311	FOI312	FOI313	FOI314	FOI315	FOI316	FOI317	FOI318	FOI319	FOI320	FOI321	FOI322	FOI323	FOI324	FOI325	FOI326	FOI327	FOI328	FOI329	FOI330	FOI331	FOI332	FOI333	FOI334	FOI335	FOI336	FOI337	FOI338	FOI339	FOI340	FOI341	FOI342	FOI343	FOI344	FOI345	FOI346	FOI347	FOI348	FOI349	FOI350	FOI351	FOI352	FOI353	FOI354	FOI355	FOI356	FOI357	FOI358	FOI359	FOI360	FOI361	FOI362	FOI363	FOI364	FOI365	FOI366	FOI367	FOI368	FOI369	FOI370	FOI371	FOI372	FOI373	FOI374	FOI375	FOI376	FOI377	FOI378	FOI379	FOI380	FOI381	FOI382	FOI383	FOI384	FOI385	FOI386	FOI387	FOI388	FOI389	FOI390	FOI391	FOI392	FOI393	FOI394	FOI395	FOI396	FOI397	FOI398	FOI399	FOI400	FOI401	FOI402	FOI403	FOI404	FOI405	FOI406	FOI407	FOI408	FOI409	FOI410	FOI411	FOI412	FOI413	FOI414	FOI415	FOI416	FOI417	FOI418	FOI419	FOI420	FOI421	FOI422	FOI423	FOI424	FOI425	FOI426	FOI427	FOI428	FOI429	FOI430	FOI431	FOI432	FOI433	FOI434	FOI435	FOI436	FOI437	FOI438	FOI439	FOI440	FOI441	FOI442	FOI443	FOI444	FOI445	FOI446	FOI447	FOI448	FOI449	FOI450	FOI451	FOI452	FOI453	FOI454	FOI455	FOI456	FOI457	FOI458	FOI459	FOI460	FOI461	FOI462	FOI463	FOI464	FOI465	FOI466	FOI467	FOI468	FOI469	FOI470	FOI471	FOI472	FOI473	FOI474	FOI475	FOI476	FOI477	FOI478	FOI479	FOI480	FOI481	FOI482	FOI483	FOI484	FOI485	FOI486	FOI487	FOI488	FOI489	FOI490	FOI491	FOI492	FOI493	FOI494	FOI495	FOI496	FOI497	FOI498	FOI499	FOI500	FOI501	FOI502	FOI503	FOI504	FOI505	FOI506	FOI507	FOI508	FOI509	FOI510	FOI511	FOI512	FOI513	FOI514	FOI515	FOI516	FOI517	FOI518	FOI519	FOI520	FOI521	FOI522	FOI523	FOI524	FOI525	FOI526	FOI527	FOI528	FOI529	FOI530	FOI531	FOI532	FOI533	FOI534	FOI535	FOI536	FOI537	FOI538	FOI539	FOI540	FOI541	FOI542	FOI543	FOI544	FOI545	FOI546	FOI547	FOI548	FOI549	FOI550	FOI551	FOI552	FOI553	FOI554	FOI555	FOI556	FOI557	FOI558	FOI559	FOI560	FOI561	FOI562	FOI563	FOI564	FOI565	FOI566	FOI567	FOI568	FOI569	FOI570	FOI571	FOI572	FOI573	FOI574	FOI575	FOI576	FOI577	FOI578	FOI579	FOI580	FOI581	FOI582	FOI583	FOI584	FOI585	FOI586	FOI587	FOI588	FOI589	FOI590	FOI591	FOI592	FOI593	FOI594	FOI595	FOI596	FOI597	FOI598	FOI599	FOI600	FOI601	FOI602	FOI603	FOI604	FOI605	FOI606	FOI607	FOI608	FOI609	FOI610	FOI611	FOI612	FOI613	FOI614	FOI615	FOI616	FOI617	FOI618	FOI619	FOI620	FOI621	FOI622	FOI623	FOI624	FOI625	FOI626	FOI627	FOI628	FOI629	FOI630	FOI631	FOI632	FOI633	FOI634	FOI635	FOI636	FOI637	FOI638	FOI639	FOI640	FOI641	FOI642	FOI643	FOI644	FOI645	FOI646	FOI647	FOI648	FOI649	FOI650	FOI651	FOI652	FOI653	FOI654	FOI655	FOI656	FOI657	FOI658	FOI659	FOI660	FOI661	FOI662	FOI663	FOI664	FOI665	FOI666	FOI667	FOI668	FOI669	FOI670	FOI671	FOI672	FOI673	FOI674	FOI675	FOI676	FOI677	FOI678	FOI679	FOI680	FOI681	FOI682	FOI683	FOI684	FOI685	FOI686	FOI687	FOI688	FOI689	FOI690	FOI691	FOI692	FOI693	FOI694	FOI695	FOI696	FOI697	FOI698	FOI699	FOI700	FOI701	FOI702	FOI703	FOI704	FOI705	FOI706	FOI707	FOI708	FOI709	FOI710	FOI711	FOI712	FOI713	FOI714	FOI715	FOI716	FOI717	FOI718	FOI719	FOI720	FOI721	FOI722	FOI723	FOI724	FOI725	FOI726	FOI727	FOI728	FOI729	FOI730	FOI731	FOI732	FOI733	FOI734	FOI735	FOI736	FOI737	FOI738	FOI739	FOI740	FOI741	FOI742	FOI743	FOI744	FOI745	FOI746	FOI747	FOI748	FOI749	FOI750	FOI751	FOI752	FOI753	FOI754	FOI755	FOI756	FOI757	FOI758	FOI759	FOI760	FOI761	FOI762	FOI763	FOI764	FOI765	FOI766	FOI767	FOI768	FOI769	FOI770	FOI771	FOI772	FOI773	FOI774	FOI775	FOI776	FOI777	FOI778	FOI779	FOI780	FOI781	FOI782	FOI783	FOI784	FOI785	FOI786	FOI787	FOI788	FOI789	FOI790	FOI791	FOI792	FOI793	FOI794	FOI795	FOI796	FOI797	FOI798	FOI799	FOI800	FOI801	FOI802	FOI803	FOI804	FOI805	FOI806	FOI807	FOI808	FOI809	FOI810	FOI811	FOI812	FOI813	FOI814	FOI815	FOI816	FOI817	FOI818	FOI819	FOI820	FOI821	FOI822	FOI823	FOI824	FOI825	FOI826	FOI827	FOI828	FOI829	FOI830	FOI831	FOI832	FOI833	FOI834	FOI835	FOI836	FOI837	FOI838	FOI839	FOI840	FOI841	FOI842	FOI843	FOI844	FOI845	FOI846	FOI847	FOI848	FOI849	FOI850	FOI851	FOI852	FOI853	FOI854	FOI855	FOI856	FOI857	FOI858	FOI859	FOI860	FOI861	FOI862	FOI863	FOI864	FOI865	FOI866	FOI867	FOI868	FOI869	FOI870	FOI871	FOI872	FOI873	FOI874	FOI875	FOI876	FOI877	FOI878	FOI879	FOI880	FOI881	FOI882	FOI883	FOI884	FOI885	FOI886	FOI887	FOI888	FOI889	FOI890	FOI891	FOI892	FOI893	FOI894	FOI895	FOI896	FOI897	FOI898	FOI899	FOI900	FOI901	FOI902	FOI903	FOI904	FOI905	FOI906	FOI907	FOI908	FOI909	FOI910	FOI911	FOI912	FOI913	FOI914	FOI915	FOI916	FOI917	FOI918	FOI919	FOI920	FOI921	FOI922	FOI923	FOI924	FOI925	FOI926	FOI927	FOI928	FOI929	FOI930	FOI931	FOI932	FOI933	FOI934	FOI935	FOI936	FOI937	FOI938	FOI939	FOI940	FOI941	FOI942	FOI943	FOI944	FOI945	FOI946	FOI947	FOI948	FOI949	FOI950	FOI951	FOI952	FOI953	FOI954	FOI955	FOI956	FOI957	FOI958	FOI959	FOI960	FOI961	FOI962	FOI963	FOI964	FOI965	FOI966	FOI967	FOI968	FOI969	FOI970	FOI971	FOI972	FOI973	FOI974	FOI975	FOI976	FOI977	FOI978	FOI979	FOI980	FOI981	FOI982	FOI983	FOI984	FOI985	FOI986	FOI987	FOI988	FOI989	FOI990	FOI991	FOI992	FOI993	FOI994	FOI995	FOI996	FOI997	FOI998	FOI999	FOI1000	FOI1001	FOI1002	FOI1003	FOI1004	FOI1005	FOI1006	FOI1007	FOI1008	FOI1009	FOI1010	FOI1011	FOI1012	FOI1013	FOI1014	FOI1015	FOI1016	FOI1017	FOI1018	FOI1019	FOI1020	FOI1021	FOI1022	FOI1023	FOI1024	FOI1025	FOI1026	FOI1027	FOI1028	FOI1029	FOI1030	FOI1031	FOI1032	FOI1033	FOI1034	FOI1035	FOI1036	FOI1037	FOI1038	FOI1039	FOI1040	FOI1041	FOI1042	FOI1043	FOI1044	FOI1045	FOI1046	FOI1047	FOI1048	FOI1049	FOI1050	FOI1051	FOI1052	FOI1053	FOI1054	FOI1055	FOI1056	FOI1057	FOI1058	FOI1059	FOI1060	FOI1061	FOI1062	FOI1063	FOI1064	FOI1065	FOI1066	FOI1067	FOI1068	FOI1069	FOI1070	FOI1071	FOI1072	FOI1073	FOI1074	FOI1075	FOI1076	FOI1077	FOI1078	FOI1079	FOI1080	FOI1081	FOI1082	FOI1083	FOI1084	FOI1085	FOI1086	FOI1087	FOI1088	FOI1089	FOI1090	FOI1091	FOI1092	FOI1093	FOI1094	FOI1095	FOI1096	FOI1097	FOI1098	FOI1099	FOI1100	FOI1101	FOI1102	FOI1103	FOI1104	FOI1105	FOI1106	FOI1107	FOI1108	FOI1109	FOI1110	FOI1111	FOI1112	FOI1113	FOI1114	FOI1115	FOI1116	FOI1117	FOI1118	FOI1119	FOI1120	FOI1121	FOI1122	FOI1123	FOI1124	FOI1125	FOI1126	FOI1127	FOI1128	FOI1129	FOI1130	FOI1131	FOI1132	FOI1133	FOI1134	FOI1135	FOI1136	FOI1137	FOI1138	FOI1139	FOI1140	FOI1141	FOI1142	FOI1143	FOI1144	FOI1145	FOI1146	FOI1147	FOI1148	FOI1149	FOI1150	FOI1151	FOI1152	FOI1153	FOI1154	FOI1155	FOI1156	FOI1157	FOI1158	FOI1159	FOI1160	FOI1161	FOI1162	FOI1163	FOI1164	FOI1165	FOI1166	FOI1167	FOI1168	FOI1169	FOI1170	FOI1171	FOI1172	FOI1173	FOI1174	FOI1175	FOI1176	FOI1177	FOI1178	FOI1179	FOI1180	FOI1181	FOI1182	FOI1183	FOI1184	FOI1185	FOI1186	FOI1187	FOI1188	FOI1189	FOI1190	FOI1191	FOI1192	FOI1193	FOI1194	FOI1195	FOI1196	FOI1197	FOI1198	FOI1199	FOI1200	FOI1201	FOI1202	FOI1203	FOI1204	FOI1205	FOI120
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SNP	A1A2	COHORT_A	SIZE	FO1	FO2	FO3	FO12	FO13	COHORT_B	SIZE	FO1B	FO2B	FO3B	FO1B	FO2B	FO3B	FO1B	FO2B	FO3B
4206	A T	HELD_FEM_ADRCASE	72	72	72	72	17	38	17	HELD_FEM_ADRCTRL	72	89	55	27	35	10			
4206	A T	HELD_ALL_ADRCASESULN	26	24	28	28	5	14	7	HELD_ALL_ADRCTRL	132	161	103	47	67	18			
4527	G A	CVD_ALL_CASE	71	114	28	28	43	28	0	CVD_ALL_CTRL	54	80	28	33	14	7			
4527	G A	HELD_FEM_BAD2	320	508	132	199	110	11	11	HELD_FEM_GOOD2	370	546	194	199	148	23			
4527	G A	HELD_MAL_CASE	12	17	7	7	6	5	1	HELD_MAL_CTRL	16	30	2	14	2	0			
4527	G A	HELD_MAL_CASE2	45	71	19	19	27	17	1	HELD_MAL_CTRL2	29	36	22	11	14	4			
4527	G A	HELD_ALL_ADRCASESULN	48	68	28	28	22	24	2	HELD_ALL_ADRCTRL	124	202	46	80	42	2			
4527	G A	HELD_ALL_CASE2	104	162	46	46	63	36	5	HELD_ALL_CTRL2	71	97	45	34	29	8			
4527	G A	HELD_ALL_ADRCASESULN	26	36	16	16	12	12	2	HELD_ALL_ADRCTRL	124	202	46	80	42	2			
4544	G A	HELD_MAL_ADRCASESULN	17	20	14	14	5	10	2	HELD_MAL_ADRCTRL	59	97	21	39	19	1			
4544	G A	HELD_MAL_ADRCASE	62	87	37	37	31	25	6	HELD_MAL_ADRCTRL	59	97	21	39	19	1			
4544	G A	HELD_ALL_ADRCASE	133	183	83	83	63	57	13	HELD_ALL_ADRCTRL	130	201	59	77	47	6			
4544	G A	HELD_ALL_ADRCASESULN	47	63	31	31	20	23	4	HELD_ALL_ADRCTRL	130	201	59	77	47	6			
4545	G A	HELD_MAL_ADRCASESULN	17	20	14	14	5	10	2	HELD_MAL_ADRCTRL	59	97	21	39	19	1			
4545	G A	HELD_MAL_ADRCASE	61	85	37	37	30	25	6	HELD_MAL_ADRCTRL	59	97	21	39	19	1			
4545	G A	HELD_ALL_ADRCASE	132	181	83	83	62	57	13	HELD_ALL_ADRCTRL	128	197	59	75	47	6			
4668	C A	HELD_ALL_ADRCASESULN	26	34	18	18	9	16	1	HELD_ALL_ADRCTRL	130	139	121	39	61	30			
4669	C T	HELD_FEM_HIRBSP	286	474	98	98	195	84	7	HELD_FEM_LORESF	281	490	72	214	62	5			
4718	G A	HELD_MAL_BAD	18	26	10	10	8	10	0	HELD_MAL_GOOD	34	41	27	16	9	9			
4818	G A	HELD_MAL_BAD	17	20	14	14	3	14	0	HELD_MAL_GOOD	36	54	18	20	14	2			
4827	A G	HELD_MAL_ADRCASESULN	9	15	3	3	7	1	1	HELD_MAL_ADRCTRL	59	103	15	44	15	0			

DaySNP	A1A2	COHORT_A	SIZE_A	FOI1A	FOI2A	FOI1A	FOI2A	COHORT_B	SIZE_B	FOI1B	FOI2B	FOI1B	FOI2B		
4838	A G	HELD_ALL_CASE2	101	113	89	32	49	20	HELD_ALL_CTRL2	71	64	78	16	32	23
4856	G A	CVD_MAL_CASE	69	0	138	69	0	0	CVD_MAL_CTRL	34	65	3	31	3	0
4868	T C	HELD_MAL_ADRCASE	62	88	36	32	24	6	HELD_MAL_ADRCTRL	59	92	26	33	26	0
4868	T C	HELD_MAL_ADRCASE3ULN	8	11	5	4	3	1	HELD_MAL_ADRCTRL	59	92	26	33	26	0
4887	C A	HELD_MAL_CASE	14	26	2	12	2	0	HELD_MAL_CTRL	18	23	13	6	11	1
4887	C A	HELD_ALL_CASE	45	75	15	31	13	1	HELD_ALL_CTRL	38	53	23	17	19	2
4912	G A	HELD_MAL_BAD	12	7	17	3	1	8	HELD_MAL_GOOD	31	34	28	15	4	12
4951	G A	HELD_ALL_ADRCASE3ULN	48	51	45	19	13	16	HELD_ALL_ADRCTRL	128	145	111	37	71	20
4951	G A	HELD_FEM_ADRCASE3ULN	31	29	33	10	9	12	HELD_FEM_ADRCTRL	69	77	61	17	43	9
4951	G A	HELD_FEM_ADRCASE5ULN	17	13	21	4	5	8	HELD_FEM_ADRCTRL	69	77	61	17	43	9
4951	G A	HELD_ALL_ADRCASE5ULN	26	22	30	7	8	11	HELD_ALL_ADRCTRL	128	145	111	37	71	20
4951	G A	HELD_FEM_ADRCASE	73	68	78	19	30	24	HELD_FEM_ADRCTRL	69	77	61	17	43	9
4951	G A	HELD_ALL_ADRCASE	135	135	135	39	57	39	HELD_ALL_ADRCTRL	128	145	111	37	71	20
4952	T C	HELD_ALL_ADRCASE3ULN	48	52	44	20	12	16	HELD_ALL_ADRCTRL	128	145	111	38	69	21
4952	T C	HELD_FEM_ADRCASE3ULN	31	30	32	11	8	12	HELD_FEM_ADRCTRL	70	80	60	19	42	9
4952	T C	HELD_FEM_ADRCASE5ULN	17	14	20	5	4	8	HELD_FEM_ADRCTRL	70	80	60	19	42	9
4952	T C	HELD_ALL_ADRCASE5ULN	26	23	29	8	7	11	HELD_ALL_ADRCTRL	128	145	111	38	69	21
4966	G A	HELD_MAL_BAD	18	27	9	9	9	0	HELD_MAL_GOOD	34	34	34	7	20	7
4966	G A	HELD_MAL_ADRCASE	61	68	54	20	28	13	HELD_MAL_ADRCTRL	59	53	65	8	37	14
4966	G A	HELD_FEM_CASE	30	25	35	4	17	9	HELD_FEM_CTRL	21	26	16	8	10	3
5019	A T	CVD_FEM_CASE	32	25	39	3	19	10	CVD_FEM_CTRL	34	43	25	17	9	8

SYNT	A1	A2	COHORT_A	SIZE_A	FOA_A	Q2A	FOI_A	QO2A	FOI2	QO22	COHORT_B	SIZE_B	FOI2_B	QO2_B	FOI_B	QO2_B
5019	A	T	HELD_ALL_CASE2	87	96	78	23	50	14	14	HELD_ALL_CTRL2	62	54	70	16	22
5019	A	T	HELD_MAL_LOHDL	18	27	9	11	5	2	2	HELD_MAL_HHDL	22	20	24	6	8
5019	A	T	HELD_ALL_BAD	86	95	77	29	37	20	20	HELD_ALL_GOOD	100	84	116	25	34
5019	A	T	HELD_MAL_CASE2	37	43	31	12	19	6	6	HELD_MAL_CTRL2	24	17	31	5	7
5165	C	A	HELD_FEM_ADRCASE5ULN	30	46	14	16	14	0	0	HELD_FEM_ADRCTRL	70	122	18	54	14
5165	C	A	HELD_MAL_ADRCASE5ULN	9	15	3	7	1	1	1	HELD_MAL_ADRCTRL	59	103	15	44	15
5165	C	A	HELD_FEM_ADRCASE	71	116	26	45	26	0	0	HELD_FEM_ADRCTRL	70	122	18	54	14
5165	C	A	HELD_FEM_ADRCASE5ULN	16	24	8	8	8	0	0	HELD_FEM_ADRCTRL	70	122	18	54	14
5278	G	A	HELD_MAL_ADRCASE5ULN	9	10	8	3	4	2	2	HELD_MAL_ADRCTRL	60	93	27	35	23
5287	C	T	HELD_FEM_VHRESF	159	257	61	108	41	10	10	HELD_FEM_VLORESF	147	260	34	116	28
5320	A	G	CVD_FEM_CASE	33	40	26	11	18	4	4	CVD_FEM_CTRL	38	32	44	9	14
5324	T	C	HELD_FEM_VHRESF	137	124	150	31	62	44	44	HELD_FEM_VLORESF	134	146	122	40	66
5373	G	T	HELD_FEM_ADRCASE5ULN	16	29	3	13	3	0	0	HELD_FEM_ADRCTRL	71	94	48	28	38
5373	G	T	HELD_ALL_ADRCASE5ULN	25	42	8	17	8	0	0	HELD_ALL_ADRCTRL	131	180	82	60	60
5375	C	T	HELD_FEM_ADRCASE5ULN	15	27	3	12	3	0	0	HELD_FEM_ADRCTRL	70	90	50	26	38
5375	C	T	HELD_ALL_ADRCASE5ULN	24	39	9	15	9	0	0	HELD_ALL_ADRCTRL	128	173	83	57	59
5376	A	T	HELD_MAL_ADRCASE5ULN	8	15	1	7	1	0	0	HELD_MAL_ADRCTRL	58	116	0	58	0
5377	T	C	HELD_FEM_ADRCASE	60	88	32	35	18	7	7	HELD_FEM_ADRCTRL	64	85	43	25	35
5377	T	C	HELD_FEM_ADRCASE5ULN	15	26	4	11	4	0	0	HELD_FEM_ADRCTRL	64	85	43	25	35
5517	A	G	HELD_MAL_ADRCASE	53	104	2	52	0	1	1	HELD_MAL_ADRCTRL	55	106	4	51	4
5518	G	C	HELD_FEM_ADRCASE5ULN	16	31	1	15	1	0	0	HELD_FEM_ADRCTRL	71	0	142	71	0

INSTR	ALIA2	COHOPI_A	SIZE_A	FO1A	FO1B	FO1C	FO1D	FO2A	COHORT_B	SIZE_B	FO1_B	FO2_B	FO1I	FO1J	FO2J
5564	G T	CVD_MAL_CASE	69	73	65	11	51	7	CVD_MAL_CTRL	34	44	24	14	16	4
5569	G A	HELD_MAL_ADRCASE5ULN	8	15	1	7	1	0	HELD_MAL_ADRCTRL	53	74	32	25	24	4
5569	G A	HELD_ALL_ADRCASE5ULN	22	37	7	15	7	0	HELD_ALL_ADRCTRL	122	170	74	60	50	12
5716	G C	HELD_ALL_ADRCASE3ULN	44	34	54	6	22	16	HELD_ALL_ADRCTRL	109	126	92	34	58	17
5716	G C	HELD_FEM_ADRCASE3ULN	29	18	40	2	14	13	HELD_FEM_ADRCTRL	59	65	53	16	33	10
5716	G C	HELD_ALL_ADRCASE5ULN	22	16	28	2	12	8	HELD_ALL_ADRCTRL	109	126	92	34	58	17
5716	G C	HELD_FEM_ADRCASE5ULN	15	10	20	1	8	6	HELD_FEM_ADRCTRL	59	65	53	16	33	10
5717	G A	HELD_ALL_ADRCASE5ULN	26	20	32	3	14	9	HELD_ALL_ADRCTRL	132	142	122	39	64	29
5717	G A	CVD_FEM_CASE	17	12	22	3	6	8	CVD_FEM_CTRL	19	22	16	5	12	2
5850	G A	HELD_MAL_CASE	14	14	14	5	4	5	HELD_MAL_CTRL	15	21	9	6	9	0
5959	G A	CVD_MAL_CASE	58	78	38	27	24	7	CVD_MAL_CTRL	29	30	28	6	18	5
6151	C A	HELD_MAL_ADRCASE	58	76	40	22	32	4	HELD_MAL_ADRCTRL	58	83	33	32	19	7
6236	T C	HELD_ALL_ADRCASE	129	177	81	67	43	19	HELD_ALL_ADRCTRL	128	193	63	72	49	7
6277	T G	HELD_FEM_ADRCASE5ULN	16	21	11	8	5	3	HELD_FEM_ADRCTRL	66	112	20	46	20	0
6277	T G	HELD_ALL_ADRCASE5ULN	23	33	13	13	7	3	HELD_ALL_ADRCTRL	124	205	43	82	41	1
6277	T G	HELD_FEM_ADRCASE	72	105	39	39	27	6	HELD_FEM_ADRCTRL	66	112	20	46	20	0
6277	T G	HELD_FEM_ADRCASE3ULN	30	42	18	15	12	3	HELD_FEM_ADRCTRL	66	112	20	46	20	0
6313	C T	HELD_FEM_UHIRESP	52	54	50	15	24	13	HELD_FEM_ULORESP	72	89	55	23	43	6
6369	T C	HELD_FEM_BAD	63	82	44	26	30	7	HELD_FEM_GOOD	68	72	64	19	34	15
6374	T C	HELD_ALL_ADRCASE3ULN	47	52	42	14	24	9	HELD_ALL_ADRCTRL	126	177	75	62	53	11
6374	T C	HELD_MAL_ADRCASE3ULN	17	15	19	3	9	5	HELD_MAL_ADRCTRL	58	79	37	28	23	7

USNSN	AL	AL2	COHORT_A	SEX	FOI_A	FOI_A1	FOI_A2	FOI_A3	FOI_A4	FOI_A5	FOI_A6	FOI_A7	FOI_A8	FOI_A9	FOI_A10	FOI_A11	FOI_A12	FOI_A13	FOI_A14	FOI_A15	FOI_A16	FOI_A17	FOI_A18	FOI_A19	FOI_A20	FOI_A21	FOI_A22	FOI_A23	FOI_A24	FOI_A25	FOI_A26	FOI_A27	FOI_A28	FOI_A29	FOI_A30	FOI_A31	FOI_A32	FOI_A33	FOI_A34	FOI_A35	FOI_A36	FOI_A37	FOI_A38	FOI_A39	FOI_A40	FOI_A41	FOI_A42	FOI_A43	FOI_A44	FOI_A45	FOI_A46	FOI_A47	FOI_A48	FOI_A49	FOI_A50	FOI_A51	FOI_A52	FOI_A53	FOI_A54	FOI_A55	FOI_A56	FOI_A57	FOI_A58	FOI_A59	FOI_A60	FOI_A61	FOI_A62	FOI_A63	FOI_A64	FOI_A65	FOI_A66	FOI_A67	FOI_A68	FOI_A69	FOI_A70	FOI_A71	FOI_A72	FOI_A73	FOI_A74	FOI_A75	FOI_A76	FOI_A77	FOI_A78	FOI_A79	FOI_A80	FOI_A81	FOI_A82	FOI_A83	FOI_A84	FOI_A85	FOI_A86	FOI_A87	FOI_A88	FOI_A89	FOI_A90	FOI_A91	FOI_A92	FOI_A93	FOI_A94	FOI_A95	FOI_A96	FOI_A97	FOI_A98	FOI_A99	FOI_A100	FOI_A101	FOI_A102	FOI_A103	FOI_A104	FOI_A105	FOI_A106	FOI_A107	FOI_A108	FOI_A109	FOI_A110	FOI_A111	FOI_A112	FOI_A113	FOI_A114	FOI_A115	FOI_A116	FOI_A117	FOI_A118	FOI_A119	FOI_A120	FOI_A121	FOI_A122	FOI_A123	FOI_A124	FOI_A125	FOI_A126	FOI_A127	FOI_A128	FOI_A129	FOI_A130	FOI_A131	FOI_A132	FOI_A133	FOI_A134	FOI_A135	FOI_A136	FOI_A137	FOI_A138	FOI_A139	FOI_A140	FOI_A141	FOI_A142	FOI_A143	FOI_A144	FOI_A145	FOI_A146	FOI_A147	FOI_A148	FOI_A149	FOI_A150	FOI_A151	FOI_A152	FOI_A153	FOI_A154	FOI_A155	FOI_A156	FOI_A157	FOI_A158	FOI_A159	FOI_A160	FOI_A161	FOI_A162	FOI_A163	FOI_A164	FOI_A165	FOI_A166	FOI_A167	FOI_A168	FOI_A169	FOI_A170	FOI_A171	FOI_A172	FOI_A173	FOI_A174	FOI_A175	FOI_A176	FOI_A177	FOI_A178	FOI_A179	FOI_A180	FOI_A181	FOI_A182	FOI_A183	FOI_A184	FOI_A185	FOI_A186	FOI_A187	FOI_A188	FOI_A189	FOI_A190	FOI_A191	FOI_A192	FOI_A193	FOI_A194	FOI_A195	FOI_A196	FOI_A197	FOI_A198	FOI_A199	FOI_A200	FOI_A201	FOI_A202	FOI_A203	FOI_A204	FOI_A205	FOI_A206	FOI_A207	FOI_A208	FOI_A209	FOI_A210	FOI_A211	FOI_A212	FOI_A213	FOI_A214	FOI_A215	FOI_A216	FOI_A217	FOI_A218	FOI_A219	FOI_A220	FOI_A221	FOI_A222	FOI_A223	FOI_A224	FOI_A225	FOI_A226	FOI_A227	FOI_A228	FOI_A229	FOI_A230	FOI_A231	FOI_A232	FOI_A233	FOI_A234	FOI_A235	FOI_A236	FOI_A237	FOI_A238	FOI_A239	FOI_A240	FOI_A241	FOI_A242	FOI_A243	FOI_A244	FOI_A245	FOI_A246	FOI_A247	FOI_A248	FOI_A249	FOI_A250	FOI_A251	FOI_A252	FOI_A253	FOI_A254	FOI_A255	FOI_A256	FOI_A257	FOI_A258	FOI_A259	FOI_A260	FOI_A261	FOI_A262	FOI_A263	FOI_A264	FOI_A265	FOI_A266	FOI_A267	FOI_A268	FOI_A269	FOI_A270	FOI_A271	FOI_A272	FOI_A273	FOI_A274	FOI_A275	FOI_A276	FOI_A277	FOI_A278	FOI_A279	FOI_A280	FOI_A281	FOI_A282	FOI_A283	FOI_A284	FOI_A285	FOI_A286	FOI_A287	FOI_A288	FOI_A289	FOI_A290	FOI_A291	FOI_A292	FOI_A293	FOI_A294	FOI_A295	FOI_A296	FOI_A297	FOI_A298	FOI_A299	FOI_A300	FOI_A301	FOI_A302	FOI_A303	FOI_A304	FOI_A305	FOI_A306	FOI_A307	FOI_A308	FOI_A309	FOI_A310	FOI_A311	FOI_A312	FOI_A313	FOI_A314	FOI_A315	FOI_A316	FOI_A317	FOI_A318	FOI_A319	FOI_A320	FOI_A321	FOI_A322	FOI_A323	FOI_A324	FOI_A325	FOI_A326	FOI_A327	FOI_A328	FOI_A329	FOI_A330	FOI_A331	FOI_A332	FOI_A333	FOI_A334	FOI_A335	FOI_A336	FOI_A337	FOI_A338	FOI_A339	FOI_A340	FOI_A341	FOI_A342	FOI_A343	FOI_A344	FOI_A345	FOI_A346	FOI_A347	FOI_A348	FOI_A349	FOI_A350	FOI_A351	FOI_A352	FOI_A353	FOI_A354	FOI_A355	FOI_A356	FOI_A357	FOI_A358	FOI_A359	FOI_A360	FOI_A361	FOI_A362	FOI_A363	FOI_A364	FOI_A365	FOI_A366	FOI_A367	FOI_A368	FOI_A369	FOI_A370	FOI_A371	FOI_A372	FOI_A373	FOI_A374	FOI_A375	FOI_A376	FOI_A377	FOI_A378	FOI_A379	FOI_A380	FOI_A381	FOI_A382	FOI_A383	FOI_A384	FOI_A385	FOI_A386	FOI_A387	FOI_A388	FOI_A389	FOI_A390	FOI_A391	FOI_A392	FOI_A393	FOI_A394	FOI_A395	FOI_A396	FOI_A397	FOI_A398	FOI_A399	FOI_A400	FOI_A401	FOI_A402	FOI_A403	FOI_A404	FOI_A405	FOI_A406	FOI_A407	FOI_A408	FOI_A409	FOI_A410	FOI_A411	FOI_A412	FOI_A413	FOI_A414	FOI_A415	FOI_A416	FOI_A417	FOI_A418	FOI_A419	FOI_A420	FOI_A421	FOI_A422	FOI_A423	FOI_A424	FOI_A425	FOI_A426	FOI_A427	FOI_A428	FOI_A429	FOI_A430	FOI_A431	FOI_A432	FOI_A433	FOI_A434	FOI_A435	FOI_A436	FOI_A437	FOI_A438	FOI_A439	FOI_A440	FOI_A441	FOI_A442	FOI_A443	FOI_A444	FOI_A445	FOI_A446	FOI_A447	FOI_A448	FOI_A449	FOI_A450	FOI_A451	FOI_A452	FOI_A453	FOI_A454	FOI_A455	FOI_A456	FOI_A457	FOI_A458	FOI_A459	FOI_A460	FOI_A461	FOI_A462	FOI_A463	FOI_A464	FOI_A465	FOI_A466	FOI_A467	FOI_A468	FOI_A469	FOI_A470	FOI_A471	FOI_A472	FOI_A473	FOI_A474	FOI_A475	FOI_A476	FOI_A477	FOI_A478	FOI_A479	FOI_A480	FOI_A481	FOI_A482	FOI_A483	FOI_A484	FOI_A485	FOI_A486	FOI_A487	FOI_A488	FOI_A489	FOI_A490	FOI_A491	FOI_A492	FOI_A493	FOI_A494	FOI_A495	FOI_A496	FOI_A497	FOI_A498	FOI_A499	FOI_A500	FOI_A501	FOI_A502	FOI_A503	FOI_A504	FOI_A505	FOI_A506	FOI_A507	FOI_A508	FOI_A509	FOI_A510	FOI_A511	FOI_A512	FOI_A513	FOI_A514	FOI_A515	FOI_A516	FOI_A517	FOI_A518	FOI_A519	FOI_A520	FOI_A521	FOI_A522	FOI_A523	FOI_A524	FOI_A525	FOI_A526	FOI_A527	FOI_A528	FOI_A529	FOI_A530	FOI_A531	FOI_A532	FOI_A533	FOI_A534	FOI_A535	FOI_A536	FOI_A537	FOI_A538	FOI_A539	FOI_A540	FOI_A541	FOI_A542	FOI_A543	FOI_A544	FOI_A545	FOI_A546	FOI_A547	FOI_A548	FOI_A549	FOI_A550	FOI_A551	FOI_A552	FOI_A553	FOI_A554	FOI_A555	FOI_A556	FOI_A557	FOI_A558	FOI_A559	FOI_A560	FOI_A561	FOI_A562	FOI_A563	FOI_A564	FOI_A565	FOI_A566	FOI_A567	FOI_A568	FOI_A569	FOI_A570	FOI_A571	FOI_A572	FOI_A573	FOI_A574	FOI_A575	FOI_A576	FOI_A577	FOI_A578	FOI_A579	FOI_A580	FOI_A581	FOI_A582	FOI_A583	FOI_A584	FOI_A585	FOI_A586	FOI_A587	FOI_A588	FOI_A589	FOI_A590	FOI_A591	FOI_A592	FOI_A593	FOI_A594	FOI_A595	FOI_A596	FOI_A597	FOI_A598	FOI_A599	FOI_A600	FOI_A601	FOI_A602	FOI_A603	FOI_A604	FOI_A605	FOI_A606	FOI_A607	FOI_A608	FOI_A609	FOI_A610	FOI_A611	FOI_A612	FOI_A613	FOI_A614	FOI_A615	FOI_A616	FOI_A617	FOI_A618	FOI_A619	FOI_A620	FOI_A621	FOI_A622	FOI_A623	FOI_A624	FOI_A625	FOI_A626	FOI_A627	FOI_A628	FOI_A629	FOI_A630	FOI_A631	FOI_A632	FOI_A633	FOI_A634	FOI_A635	FOI_A636	FOI_A637	FOI_A638	FOI_A639	FOI_A640	FOI_A641	FOI_A642	FOI_A643	FOI_A644	FOI_A645	FOI_A646	FOI_A647	FOI_A648	FOI_A649	FOI_A650	FOI_A651	FOI_A652	FOI_A653	FOI_A654	FOI_A655	FOI_A656	FOI_A657	FOI_A658	FOI_A659	FOI_A660	FOI_A661	FOI_A662	FOI_A663	FOI_A664	FOI_A665	FOI_A666	FOI_A667	FOI_A668	FOI_A669	FOI_A670	FOI_A671	FOI_A672	FOI_A673	FOI_A674	FOI_A675	FOI_A676	FOI_A677	FOI_A678	FOI_A679	FOI_A680	FOI_A681	FOI_A682	FOI_A683	FOI_A684	FOI_A685	FOI_A686	FOI_A687	FOI_A688	FOI_A689	FOI_A690	FOI_A691	FOI_A692	FOI_A693	FOI_A694	FOI_A695	FOI_A696	FOI_A697	FOI_A698	FOI_A699	FOI_A700	FOI_A701	FOI_A702	FOI_A703	FOI_A704	FOI_A705	FOI_A706	FOI_A707	FOI_A708	FOI_A709	FOI_A710	FOI_A711	FOI_A712	FOI_A713	FOI_A714	FOI_A715	FOI_A716	FOI_A717	FOI_A718	FOI_A719	FOI_A720	FOI_A721	FOI_A722	FOI_A723	FOI_A724	FOI_A725	FOI_A726	FOI_A727	FOI_A728	FOI_A729	FOI_A730	FOI_A731	FOI_A732	FOI_A733	FOI_A734	FOI_A735	FOI_A736	FOI_A737	FOI_A738	FOI_A739	FOI_A740	FOI_A741	FOI_A742	FOI_A743	FOI_A744	FOI_A745	FOI_A746	FOI_A747	FOI_A748	FOI_A749	FOI_A750	FOI_A751	FOI_A752	FOI_A753	FOI_A754	FOI_A755	FOI_A756	FOI_A757	FOI_A758	FOI_A759	FOI_A760	FOI_A761	FOI_A762	FOI_A763	FOI_A764	FOI_A765	FOI_A766	FOI_A767	FOI_A768	FOI_A769	FOI_A770	FOI_A771	FOI_A772	FOI_A773	FOI_A774	FOI_A775	FOI_A776	FOI_A777	FOI_A778	FOI_A779	FOI_A780	FOI_A781	FOI_A782	FOI_A783	FOI_A784	FOI_A785	FOI_A786	FOI_A787	FOI_A788	FOI_A789	FOI_A790	FOI_A791	FOI_A792	FOI_A793	FOI_A794	FOI_A795	FOI_A796	FOI_A797	FOI_A798	FOI_A799	FOI_A800	FOI_A801	FOI_A802	FOI_A803	FOI_A804	FOI_A805	FOI_A806	FOI_A807	FOI_A808	FOI_A809	FOI_A810	FOI_A811	FOI_A812	FOI_A813	FOI_A814	FOI_A815	FOI_A816	FOI_A817	FOI_A818	FOI_A819	FOI_A820	FOI_A821	FOI_A822	FOI_A823	FOI_A824	FOI_A825	FOI_A826	FOI_A827	FOI_A828	FOI_A829	FOI_A830	FOI_A831	FOI_A832	FOI_A833	FOI_A834	FOI_A835	FOI_A836	FOI_A837	FOI_A838	FOI_A839	FOI_A840	FOI_A841	FOI_A842	FOI_A843	FOI_A844	FOI_A845	FOI_A846	FOI_A847	FOI_A848	FOI_A849	FOI_A850	FOI_A851	FOI_A852	FOI_A853	FOI_A854	FOI_A855	FOI_A856	FOI_A857	FOI_A858	FOI_A859	FOI_A860	FOI_A861	FOI_A862	FOI_A863	FOI_A864	FOI_A865	FOI_A866	FOI_A867	FOI_A868	FOI_A869	FOI_A870	FOI_A871	FOI_A872	FOI_A873	FOI_A874	FOI_A875	FOI_A876	FOI_A877	FOI_A878	FOI_A879	FOI_A880	FOI_A881	FOI_A882	FOI_A883	FOI_A884	FOI_A885	FOI_A886	FOI_A887	FOI_A888	FOI_A889	FOI_A890	FOI_A891	FOI_A892	FOI_A893	FOI_A894	FOI_A895	FOI_A896	FOI_A897	FOI_A898	FOI_A899	FOI_A900	FOI_A901	FOI_A902	FOI_A903	FOI_A904	FOI_A905	FOI_A906	FOI_A907	FOI_A908	FOI_A909	FOI_A910	FOI_A911	FOI_A912	FOI_A913	FOI_A914	FOI_A915	FOI_A916	FOI_A917	FOI_A918	FOI_A919	FOI_A920	FOI_A921	FOI_A922	FOI_A923	FOI_A924	FOI_A925	FOI_A926	FOI_A927	FOI_A928	FOI_A929	FOI_A930	FOI_A931	FOI_A932	FOI_A933	FOI_A934	FOI_A935	FOI_A936	FOI_A937	FOI_A938	FOI_A939	FOI_A940	FOI_A941	FOI_A942	FOI_A943	FOI_A944	FOI_A945	FOI_A946	FOI_A947	FOI_A948	FOI_A949	FOI_A950	FOI_A951	FOI_A952	FOI_A953	FOI_A954	FOI_A955	FOI_A956	FOI_A957	FOI_A958	FOI_A959	FOI_A960	FOI_A961	FOI_A962	FOI_A963	FOI_A964	FOI_A965	FOI_A966	FOI_A967	FOI_A968	FOI_A969	FOI_A970	FOI_A971	FOI_A972	FOI_A973	FOI_A974	FOI_A975	FOI_A976	FOI_A977	FOI_A978	FOI_A979	FOI_A980	FOI_A981	FOI_A982	FOI_A983	FOI_A984	FOI_A985	FOI_A986	FOI_A987	FOI_A988	FOI_A989	FOI_A990	FOI_A991	FOI_A992	FOI_A993	FOI_A994	FOI_A995	FOI_A996	FOI_A997	FOI_A998	FOI_A999	FOI_A1000	FOI_A1001	FOI_A1002	FOI_A1003	FOI_A1004	FOI_A1005	FOI_A1006	FOI_A1007	FOI_A1008	FOI_A1009	FOI_A1010	FOI_A1011	FOI_A1012	FOI_A1013	FOI_A1014	FOI_A1015	FOI_A1016	FOI_A1017	FOI_A1018	FOI_A1019	FOI_A1020	FOI_A1021	FOI_A1022	FOI_A1023	FOI_A1024	FOI_A1025	FOI_A1026	FOI_A1027	FOI_A1028	FOI_A1029	FOI_A1030	FOI_A1031	FOI_A1032	FOI_A1033	FOI_A1034	FOI_A1035	FOI_A1036	FOI_A1037	FOI_A1038	FOI_A1039	FOI_A1040	FOI_A1041	FOI_A1042	FOI_A1043	FOI_A1044	FOI_A1045	FOI_A1046	FOI_A1047	FOI_A1048	FOI_A1049	FOI_A1050	FOI_A1051	FOI_A1052	FOI_A1053	FOI_A1054	FOI_A1055	FOI_A1056	FOI_A1057	FOI_A1058	FOI_A1059	FOI_A1060	FOI_A1061	FOI_A1062	FOI_A1063	FOI_A1064	FOI_A1065	FOI_A1066	FOI_A1067	FOI_A1068	FOI_A1069	FOI_A1070	FOI_A1071	FOI_A1072	FOI_A1073	FOI_A1074	FOI_A1075	FOI_A1076	FOI_A1077	FOI_A1078	FOI_A1079	FOI_A1080	FOI_A1081	FOI_A1082	FOI_A1083	FOI_A1084	FOI_A1085	FOI_A1086	FOI_A1087	FOI_A1088	FOI_A1089	FOI_A1090	FOI_A1091	FOI_A1092	FOI_A1093	FOI_A1094	FOI_A1095	FOI_A1096	FOI_A1097	FOI_A1098	FOI_A1099	FOI_A1100	FOI_A1101	FOI_A1102	FOI_A1103	FOI_A1104	FOI_A1105	FOI_A1106	FOI_A1107	FOI_A1108	FOI_A1109	FOI_A1110	FOI_A1111	FOI_A1112	FOI_A1113	FOI_A1114	FOI_A1115	FOI_A1116	FOI_A1117	FOI_A1118	FOI_A1119	FOI_A1120	FOI
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BRND	A1 A2	COHORT_A	SIZE	FOA_A	FOA_B	FOH_A	FOH_B	FOI2_A	FOI2_B	COHORT_B	SIZE	FOI_B	FOI_B	FOH_B	FOI2_B	FOI2_B
7128	C T	HELD_FEM_ADRCASE3ULN	28	47	9	21	5	2	2	HELD_FEM_ADRCTRL	59	77	41	25	27	7
7128	C T	HELD_ALL_ADRCASE3ULN	23	39	7	17	5	1	1	HELD_ALL_ADRCTRL	114	157	71	55	47	12
7128	C T	HELD_FEM_ADRCASE	66	101	31	42	17	7	7	HELD_FEM_ADRCTRL	59	77	41	25	27	7
7128	C T	HELD_FEM_ADRCASE3ULN	15	25	5	11	3	1	1	HELD_FEM_ADRCTRL	59	77	41	25	27	7
7363	G A	HELD_FEM_BAD	81	113	49	39	35	7	7	HELD_FEM_GOOD	79	127	31	50	27	2
7363	G A	HELD_ALL_BAD	100	143	57	51	41	8	8	HELD_ALL_GOOD	115	185	45	73	39	3
7409	A G	HELD_FEM_ADRCASE3ULN	17	24	10	8	3	1	1	HELD_FEM_ADRCTRL	72	130	14	58	14	0
7409	A G	HELD_FEM_ADRCASE3ULN	31	48	14	18	12	1	1	HELD_FEM_ADRCTRL	72	130	14	58	14	0
7409	A G	HELD_MAL_ADRCASE3ULN	7	14	0	7	0	0	0	HELD_MAL_ADRCTRL	59	95	23	39	17	3
8138	T C	HELD_MAL_BAD	19	28	10	11	6	2	2	HELD_MAL_GOOD	35	33	37	7	19	9
8138	T C	HELD_MAL_CASE	14	16	12	3	10	1	1	HELD_MAL_CTRL	19	18	20	7	4	8
8138	T C	HELD_ALL_BAD	94	112	76	38	36	20	20	HELD_ALL_GOOD	114	116	112	28	60	26
8168	C A	HELD_MAL_BAD	19	28	10	10	3	1	1	HELD_MAL_GOOD	36	66	6	31	4	1
8168	C A	HELD_FEM_BAD	79	136	22	61	14	4	4	HELD_FEM_GOOD	79	125	33	48	29	2
8210	G A	HELD_ALL_ADRCASE3ULN	46	53	39	19	15	12	12	HELD_ALL_ADRCTRL	124	147	101	38	71	15
8210	G A	HELD_FEM_ADRCASE3ULN	29	30	28	10	10	9	9	HELD_FEM_ADRCTRL	67	78	56	18	42	7
8210	G A	HELD_FEM_ADRCASE	69	70	68	20	30	19	19	HELD_FEM_ADRCTRL	67	78	56	18	42	7
8210	G A	HELD_ALL_ADRCASE	127	137	117	41	55	31	31	HELD_ALL_ADRCTRL	124	147	101	38	71	15
8241	A G	HELD_FEM_BAD	76	136	16	60	16	0	0	HELD_FEM_GOOD	77	120	34	47	26	4
8241	A G	HELD_ALL_BAD	95	166	24	74	18	3	3	HELD_ALL_GOOD	112	179	45	74	31	7
8249	C T	HELD_ALL_ADRCASE3ULN	48	86	10	38	10	0	0	HELD_ALL_ADRCTRL	129	246	12	117	12	0

INSTR	AI A2	COHORT_A	SIZE	FOUO_A	FOUO_B	FOUO_C	FOUO_D	FOUO_E	FOUO_F	COHORT_B	SIZE	FOUO_B	FOUO_B	FOUO_B	FOUO_B	FOUO_B	FOUO_B	FOUO_B	FOUO_B	FOUO_B
8249	C T	HELD_ALL_ADRCASE3ULN	26	46	6	20	6	0	HELD_ALL_ADRCTRL	129	246	12	117	12	0					
8480	C G	CVD_FEM_CASE	27	48	6	23	2	2	CVD_FEM_CTRL	39	78	0	39	0	0					
8480	C G	CVD_MAL_CASE	54	99	9	48	3	3	CVD_MAL_CTRL	34	68	0	34	0	0					
8577	T C	HELD_ALL_ADRCASE3ULN	47	50	44	12	26	9	HELD_ALL_ADRCTRL	126	167	85	56	55	15					
8577	T C	HELD_ALL_ADRCASE	132	151	113	41	69	22	HELD_ALL_ADRCTRL	126	167	85	56	55	15					
8577	T C	HELD_ALL_ADRCASE5ULN	26	27	25	7	13	6	HELD_ALL_ADRCTRL	126	167	85	56	55	15					
8578	G A	HELD_ALL_ADRCASE3ULN	48	51	45	12	27	9	HELD_ALL_ADRCTRL	130	169	91	56	57	17					
8653	C T	HELD_MAL_ADRCASE	47	87	7	40	7	0	HELD_MAL_ADRCTRL	52	81	23	29	23	0					
8653	C T	HELD_MAL_ADRCASE3ULN	14	27	1	13	1	0	HELD_MAL_ADRCTRL	52	81	23	29	23	0					
8653	C T	HELD_MAL_ADRCASE5ULN	7	14	0	7	0	0	HELD_MAL_ADRCTRL	52	81	23	29	23	0					
8653	C T	HELD_ALL_ADRCASE3ULN	41	74	8	34	6	1	HELD_ALL_ADRCTRL	114	187	41	74	39	1					
8816	G C	HELD_FEM_BAD2	315	403	227	125	153	37	HELD_FEM_GOOD2	370	419	321	122	175	73					
8816	G C	HELD_FEM_LOHDL	18	24	12	7	10	1	HELD_FEM_HIHDL	22	17	27	2	13	7					
8816	G C	HELD_ALL_CASE2	90	121	59	46	29	15	HELD_ALL_CTRL2	70	78	62	21	36	13					
8816	G C	CVD_ALL_CASE	92	138	46	57	24	11	CVD_ALL_CTRL	65	111	19	51	9	5					
8816	G C	HELD_FEM_CASE2	52	71	33	27	17	8	HELD_FEM_CTRL2	42	44	40	12	20	10					
8816	G C	HELD_MAL_LOHDL	18	22	14	7	8	3	HELD_MAL_HIHDL	17	21	13	4	13	0					
8931	C T	HELD_FEM_ADRCASE3ULN	23	43	3	21	1	1	HELD_FBM_ADRCTRL	42	70	14	29	12	1					
8943	A C	HELD_MAL_ADRCASE3ULN	16	30	2	14	2	0	HELD_MAL_ADRCTRL	55	85	25	33	19	3					
9243	C G	HELD_FEM_VHIRESP	139	230	48	92	46	1	HELD_FEM_VLORESPP	143	223	63	89	45	9					
9243	C G	HELD_MAL_ADRCASE5ULN	9	16	2	8	0	1	HELD_MAL_ADRCTRL	60	91	29	35	21	4					

DAYSNP	A1 A2	COHORT_A	SIZE_A	FO1A	FO2A	FO1F	FO12	FO22	COHORT_B	SIZE_B	FO1B	FO2B	FO1H	FO2H	FO1D
9243	C G	HELD_FEM_UHRESP	54	90	18	36	13	0	HELD_FEM_ULORESP	74	113	35	45	23	6
9523	G A	HELD_MAL_ADRCASESULN	8	12	4	4	4	0	HELD_MAL_ADRCTRL	60	109	11	49	11	0
9940	C T	HELD_MAL_CASE	12	24	0	12	0	0	HELD_MAL_CTRL	14	23	5	9	5	0
9940	C T	HELD_ALL_CASE	38	71	5	34	3	1	HELD_ALL_CTRL	31	50	12	20	10	1
10091	T C	HELD_ALL_ADRCASE3ULN	48	74	22	28	13	2	HELD_ALL_ADRCTRL	129	222	36	94	34	1
10541	G C	HELD_FEM_UHRESP	55	103	7	49	5	1	HELD_FEM_ULORESP	77	131	23	55	21	1
10541	G C	HELD_FEM_VHRESP	151	283	19	133	17	1	HELD_FEM_VLORESP	145	256	34	113	30	2
10600	G A	CVD_MAL_CASE	67	0	134	67	0	0	CVD_MAL_CTRL	34	64	4	31	2	1
10600	G A	HELD_ALL_LOHDL	39	0	78	39	0	0	HELD_ALL_HHDL	47	88	6	41	6	0
10600	G A	HELD_MAL_LOHDL	19	0	38	19	0	0	HELD_MAL_HHDL	23	42	4	19	4	0
10745	G A	HELD_MAL_BAD	19	32	6	14	4	1	HELD_MAL_GOOD	35	47	23	15	17	3
10748	T C	HELD_MAL_BAD	13	15	11	4	7	2	HELD_MAL_GOOD	30	47	13	19	9	2
10749	C G	HELD_FEM_BAD	81	124	38	46	32	3	HELD_FEM_GOOD	77	100	54	32	36	9
10785	T C	CVD_MAL_CASE	69	128	10	60	8	1	CVD_MAL_CTRL	33	55	11	23	9	1
10811	A G	HELD_FEM_BAD2	243	382	104	148	86	9	HELD_FEM_GOOD2	300	440	160	154	132	14
10811	A G	CVD_ALL_CASE	103	155	51	58	39	6	CVD_ALL_CTRL	74	124	24	53	18	3
10830	G A	HELD_ALL_BAD2	637	723	551	203	317	117	HELD_ALL_GOOD2	725	742	708	201	340	184
10830	G A	HELD_ALL_BAD	99	113	85	34	45	20	HELD_ALL_GOOD	114	98	130	22	54	38
10830	G A	HELD_MAL_BAD2	314	357	271	101	155	58	HELD_MAL_GOOD2	347	346	348	88	170	89
10830	G A	CVD_FEM_CASE	35	44	26	13	18	4	CVD_FEM_CTRL	39	33	45	5	23	11
10830	G A	HELD_MAL_BAD	19	24	14	7	10	2	HELD_MAL_GOOD	36	29	43	6	17	13

STUDY	COHORT_A	SIZE_A	FO1_A	FO2_A	FO10_A	FO11_A	FO12_A	COHORT_B	SIZE_B	FO1_B	FO2_B	FO11_B	FO12_B	FO13_B	FO14_B	FO15_B	FO16_B
10830	HELD_FEM_BAD	80	89	71	27	35	18	HELD_FEM_GOOD	78	69	87	16	37	25			
10949	HELD_FEM_VHRESP	140	163	117	45	73	22	HELD_FEM_VLORESP	143	191	95	66	59	18			
10949	HELD_FEM_HIRESP	269	319	219	92	135	42	HELD_FEM_LORESP	282	369	195	123	123	36			
10962	CVD_FEM_CASE	18	2	34	0	2	16	CVD_FEM_CTRL	18	9	27	0	9	9			
10962	HELD_ALL_ADRCASE3ULN	47	75	19	28	19	0	HELD_ALL_ADRCTRL	117	173	61	65	43	9			
10966	HELD_ALL_ADRCASE3ULN	47	74	20	27	20	0	HELD_ALL_ADRCTRL	126	179	73	63	53	10			
10966	HELD_ALL_ADRCASE5ULN	25	42	8	17	8	0	HELD_ALL_ADRCTRL	126	179	73	63	53	10			
11000	HELD_MAL_BAD2	313	483	143	187	109	17	HELD_MAL_GOOD2	348	495	201	174	147	27			
11000	CVD_FEM_CASE	35	54	16	20	14	1	CVD_FEM_CTRL	40	62	18	28	6	6			
11000	HELD_MAL_ADRCASE3ULN	17	18	16	4	10	3	HELD_MAL_ADRCTRL	60	87	33	29	29	2			
11000	HELD_ALL_BAD2	630	973	287	375	223	32	HELD_ALL_GOOD2	725	1069	381	390	289	46			
11000	HELD_MAL_ADRCASE5ULN	9	9	9	2	5	2	HELD_MAL_ADRCTRL	60	87	33	29	29	2			
11001	HELD_MAL_BAD2	309	476	142	185	106	18	HELD_MAL_GOOD2	333	471	195	165	141	27			
11001	HELD_ALL_BAD2	620	960	280	372	216	32	HELD_ALL_GOOD2	709	1044	374	381	282	46			
11001	CVD_FEM_CASE	34	52	16	19	14	1	CVD_FEM_CTRL	40	61	19	27	7	6			
11001	HELD_MAL_ADRCASE3ULN	17	18	16	4	10	3	HELD_MAL_ADRCTRL	60	87	33	29	29	2			
11001	HELD_ALL_BAD	102	163	41	64	35	3	HELD_ALL_GOOD	115	165	65	60	45	10			
11020	HELD_MAL_ADRCASE3ULN	15	25	5	10	5	0	HELD_MAL_ADRCTRL	58	76	40	25	26	7			
11073	HELD_FEM_BAD	79	90	68	26	38	15	HELD_FEM_GOOD	78	107	49	37	33	8			
11073	HELD_ALL_CASE2	106	134	78	43	48	15	HELD_ALL_CTRL2	68	100	36	39	22	7			
11192	HELD_FEM_ADRCASE5ULN	16	20	12	8	4	4	HELD_FEM_ADRCTRL	70	101	39	34	33	3			

SNP	AI	A2	COHORT_A	SIZE	FOA	FOI	FOI1	FOI2	FOI3	FOI4	FOI5	FOI6	FOI7	FOI8	FOI9	FOI10	FOI11	FOI12	FOI13	FOI14	FOI15	FOI16	FOI17	FOI18	FOI19	FOI20
11537	A	G	HELD_MAL_ADRCASE	63	93	33	36	21	6	HELD_MAL_ADRCTRL	60	101	19	43	15	2										
11558	A	C	HELD_MAL_BAD2	313	502	124	196	110	7	HELD_MAL_GOOD2	347	596	98	258	80	9										
11558	A	C	HELD_ALL_BAD2	633	1036	230	422	192	19	HELD_ALL_GOOD2	722	1239	205	535	169	18										
11558	A	C	HELD_ALL_CASE	45	81	9	38	5	2	HELD_ALL_CTRL	40	65	15	26	13	1										
11585	G	T	HELD_MAL_CASE	14	22	6	8	6	0	HELD_MAL_CTRL	18	17	19	5	7	6										
11594	T	C	HELD_ALL_ADRCASE3ULN	46	91	1	45	1	0	HELD_ALL_ADRCTRL	127	234	20	109	16	2										
11594	T	C	HELD_MAL_ADRCASE	61	119	3	58	3	0	HELD_MAL_ADRCTRL	58	106	10	48	10	0										
11614	T	C	HELD_FEM_CASE	31	52	10	21	10	0	HELD_FEM_CTRL	22	30	14	12	6	4										
11614	T	C	HELD_MAL_CASE2	48	84	12	36	12	0	HELD_MAL_CTRL2	29	43	15	17	9	3										
11614	T	C	HELD_ALL_CASE	45	74	16	29	16	0	HELD_ALL_CTRL	40	60	20	24	12	4										
11614	T	C	HELD_ALL_LOHDL	45	76	14	35	6	4	HELD_ALL_HHDL	59	99	19	41	17	1										
11631	G	A	HELD_MAL_ADRCASE5ULN	9	8	10	1	6	2	HELD_MAL_ADRCTRL	59	87	31	32	23	4										
11631	G	A	HELD_MAL_ADRCASE3ULN	17	19	15	5	9	3	HELD_MAL_ADRCTRL	59	87	31	32	23	4										
11637	A	C	HELD_FEM_BAD	77	101	53	36	29	12	HELD_FEM_GOOD	79	121	37	44	33	2										
11637	A	C	HELD_ALL_BAD	96	123	69	42	39	15	HELD_ALL_GOOD	114	171	57	63	45	6										
11637	A	C	CVD_MAL_CASE	69	111	27	44	23	2	CVD_MAL_CTRL	34	45	23	15	15	4										
11637	A	C	CVD_ALL_CASE	105	169	41	67	35	3	CVD_ALL_CTRL	74	104	44	36	32	6										
11641	G	C	HELD_MAL_ADRCASE	60	74	46	24	26	10	HELD_MAL_ADRCTRL	57	59	55	10	39	8										
11645	G	A	HELD_FEM_CASE	31	60	2	29	2	0	HELD_FEM_CTRL	22	38	6	16	6	0										
11646	C	T	HELD_FEM_BAD	81	122	40	48	26	7	HELD_FEM_GOOD	79	102	56	33	36	10										
11646	C	T	HELD_ALL_BAD	100	150	50	58	34	8	HELD_ALL_GOOD	115	152	78	49	54	12										

baySNP	AI A2	COHORT_A	SIZE_A	FO1A	FO2A	FO1B	FO2B	FO1C	FO2C	COHORT_B	SIZE_B	FO1B	FO2B	FO1C	FO2C
11652	C T	HELD_MAL_BAD	19	22	16	5	12	2	2	HELD_MAL_GOOD	35	40	30	15	10
11727	G A	HELD_ALL_ADRCASE5ULN	20	0	40	20	0	0	0	HELD_ALL_ADRCTRL	104	170	38	71	28
11727	G A	HELD_MAL_ADRCASE5ULN	13	0	26	13	0	0	0	HELD_MAL_ADRCTRL	46	68	24	26	16
11727	G A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	0	HELD_MAL_ADRCTRL	46	68	24	26	16
11727	G A	HELD_ALL_ADRCASE5ULN	37	70	4	33	4	0	0	HELD_ALL_ADRCTRL	104	170	38	71	28
11727	G A	HELD_FEM_ADRCASE5ULN	12	0	24	12	0	0	0	HELD_FEM_ADRCTRL	58	102	14	45	12
11728	T C	HELD_ALL_ADRCASE5ULN	24	44	4	20	4	0	0	HELD_ALL_ADRCTRL	128	205	51	81	43
11914	A T	HELD_MAL_ADRCASE5ULN	15	10	20	5	0	10	10	HELD_MAL_ADRCTRL	56	63	49	31	1
11938	T C	HELD_ALL_ADRCASE5ULN	48	64	32	18	23	2	2	HELD_ALL_ADRCTRL	132	163	101	57	49
11938	T C	HELD_ALL_ADRCASE5ULN	26	33	19	8	17	1	1	HELD_ALL_ADRCTRL	132	163	101	57	49
11938	T C	HELD_FEM_ADRCASE5ULN	31	38	24	9	20	2	2	HELD_FEM_ADRCTRL	72	83	61	27	29
11950	G A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	0	HELD_MAL_ADRCTRL	55	78	32	26	26
11950	G A	HELD_MAL_ADRCASE5ULN	15	27	3	13	1	1	1	HELD_MAL_ADRCTRL	55	78	32	26	26
11950	G A	HELD_MAL_ADRCASE	55	84	26	35	14	6	6	HELD_MAL_ADRCTRL	55	78	32	26	26
11951	G A	HELD_MAL_ADRCASE5ULN	7	0	14	7	0	0	0	HELD_MAL_ADRCTRL	58	84	32	29	26
11951	G A	HELD_FEM_UHRESP	55	82	28	32	13	5	5	HELD_FEM_ULORESP	76	127	25	51	25
12008	C T	HELD_ALL_ADRCASE	119	234	4	115	4	0	0	HELD_ALL_ADRCTRL	113	215	11	102	11
12031	A G	HELD_ALL_ADRCASE5ULN	47	51	43	19	13	15	15	HELD_ALL_ADRCTRL	126	144	108	37	70
12031	A G	HELD_FEM_ADRCASE5ULN	17	13	21	4	5	8	8	HELD_FEM_ADRCTRL	70	79	61	18	43
12031	A G	HELD_ALL_ADRCASE5ULN	26	22	30	7	8	11	11	HELD_ALL_ADRCTRL	126	144	108	37	70
12031	A G	HELD_FEM_ADRCASE5ULN	30	29	31	10	9	11	11	HELD_FEM_ADRCTRL	70	79	61	18	43

SNP	A142	COHORT_A	SIZE	FOI_A	FOI_B	FOI12	FOI13	FOI14	FOI15	FOI16	FOI17	FOI18	FOI19	FOI20	FOI21	FOI22
12031	A	G	HELD_ALL_ADRCASE	133	133	133	39	55	39	HELD_ALL_ADRCTRL	126	144	108	37	70	19
12031	A	G	HELD_FEM_ADRCASE	72	68	76	19	30	23	HELD_FEM_ADRCTRL	70	79	61	18	43	9
12032	T	C	HELD_FEM_UHIRESP	51	88	14	38	12	1	HELD_FEM_ULORESP	71	136	6	65	6	0
12032	T	C	HELD_FEM_ADRCASE	73	130	16	59	12	2	HELD_FEM_ADRCTRL	70	134	6	64	6	0
12032	T	C	HELD_ALL_ADRCASE	134	240	28	109	22	3	HELD_ALL_ADRCTRL	128	242	14	114	14	0
12032	T	C	HELD_FEM_VHIRESP	136	243	29	108	27	1	HELD_FEM_VLORESP	140	262	18	124	14	2
12148	G	A	HELD_MAL_ADRCASE5ULN	8	7	9	1	5	2	HELD_MAL_ADRCTRL	55	83	27	30	23	2
12148	G	A	HELD_MAL_ADRCASE	55	66	44	19	28	8	HELD_MAL_ADRCTRL	55	83	27	30	23	2
12148	G	A	HELD_MAL_ADRCASE3ULN	16	18	14	5	8	3	HELD_MAL_ADRCTRL	55	83	27	30	23	2
12207	A	G	HELD_MAL_ADRCASE5ULN	9	12	6	6	0	3	HELD_MAL_ADRCTRL	58	84	32	29	26	3
12207	A	G	HELD_MAL_ADRCASE	59	74	44	30	14	15	HELD_MAL_ADRCTRL	58	84	32	29	26	3
12207	A	G	HELD_MAL_ADRCASE3ULN	17	23	11	10	3	4	HELD_MAL_ADRCTRL	58	84	32	29	26	3
12399	A	G	HELD_MAL_ADRCASE5ULN	8	11	5	3	5	0	HELD_MAL_ADRCTRL	60	106	14	46	14	0
12399	A	G	HELD_MAL_ADRCASE3ULN	16	24	8	8	8	0	HELD_MAL_ADRCTRL	60	106	14	46	14	0
12399	A	G	HELD_ALL_ADRCASE	132	217	47	89	39	4	HELD_ALL_ADRCTRL	131	232	30	103	26	2
12554	A	T	HELD_MAL_ADRCASE	62	98	26	37	24	1	HELD_MAL_ADRCTRL	55	99	11	44	11	0
12554	A	T	HELD_FEM_VHIRESP	151	234	68	88	58	5	HELD_FEM_VLORESP	144	243	45	102	39	3
12851	T	C	HELD_FEM_ADRCASE5ULN	17	22	12	6	10	1	HELD_FEM_ADRCTRL	71	115	27	46	23	2
12851	T	C	HELD_MAL_ADRCASE	62	94	30	34	26	2	HELD_MAL_ADRCTRL	60	88	32	36	16	8
13025	A	C	HELD_MAL_ADRCASE5ULN	17	24	10	11	2	4	HELD_MAL_ADRCTRL	58	80	36	28	24	6
13025	A	C	HELD_FEM_ADRCASE5ULN	17	19	15	7	5	5	HELD_FEM_ADRCTRL	70	93	47	29	35	6

db/SNP	A1	A2	COHORT_A	SIZE	FO1	FO2_A	FO14	FO12	FO22	COHORT_B	SIZE	FO1B	FO2B	FO1	FO2	FO17	FO27
13191	G	A	HELD_ALL_CASE	43	50	36	16	18	9	HELD_ALL_CTRL	39	58	20	21	16	2	
13192	T	C	HELD_MAL_ADRCASE3ULN	17	25	9	11	3	3	HELD_MAL_ADRCTRL	59	97	21	38	21	0	
13192	T	C	HELD_MAL_ADRCASE5ULN	9	14	4	6	2	1	HELD_MAL_ADRCTRL	59	97	21	38	21	0	
13192	T	C	HELD_ALL_ADRCASE3ULN	47	77	17	33	11	3	HELD_ALL_ADRCTRL	129	212	46	84	44	1	
13192	T	C	HELD_MAL_ADRCASE	61	98	24	41	16	4	HELD_MAL_ADRCTRL	59	97	21	38	21	0	
13193	G	A	HELD_MAL_ADRCASE3ULN	16	23	9	10	3	3	HELD_MAL_ADRCTRL	58	94	22	36	22	0	
13193	G	A	HELD_MAL_ADRCASE5ULN	8	12	4	5	2	1	HELD_MAL_ADRCTRL	58	94	22	36	22	0	
13193	G	A	HELD_ALL_ADRCASE3ULN	47	77	17	33	11	3	HELD_ALL_ADRCTRL	130	212	48	83	46	1	
13338	G	A	HELD_FEM_UHIRESP	55	75	35	23	29	3	HELD_FEM_ULORESP	71	92	50	34	24	13	
13338	G	A	HELD_FEM_VHIRESP	148	187	109	58	71	19	HELD_FEM_VLORESP	139	178	100	66	46	27	
13339	G	A	HELD_MAL_ADRCASE	50	42	58	0	42	8	HELD_MAL_ADRCTRL	50	47	53	6	35	9	
13339	G	A	CVD_FEM_CASE	31	57	5	26	5	0	CVD_FEM_CTRL	35	56	14	22	12	1	
13340	C	A	HELD_FEM_VHIRESP	21	21	21	4	13	4	HELD_FEM_VLORESP	17	27	7	11	5	1	
13479	G	A	HELD_FEM_UHIRESP	48	73	23	28	17	3	HELD_FEM_ULORESP	65	113	17	50	13	2	
13633	T	C	HELD_FEM_ADRCASE3ULN	27	36	18	12	12	3	HELD_FEM_ADRCTRL	69	112	26	45	22	2	
13633	T	C	HELD_FEM_ADRCASE	64	90	38	32	26	6	HELD_FEM_ADRCTRL	69	112	26	45	22	2	
13929	G	A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	54	94	14	41	12	1	
14065	C	T	HELD_FEM_HIRESP	267	473	61	208	57	2	HELD_FEM_LORESP	271	501	41	231	39	1	
14083	T	C	HELD_FEM_ADRCASE	69	123	15	54	15	0	HELD_FEM_ADRCTRL	70	112	28	46	20	4	
14085	T	C	HELD_FEM_HIRESP	240	405	75	168	69	3	HELD_FEM_LORESP	230	404	56	180	44	6	
14087	T	C	HELD_FEM_HIRESP	268	452	84	188	76	4	HELD_FEM_LORESP	283	496	70	220	56	7	

STAFFNO	AT02	COHORT_A	SIZE_A	HOLD_MAL_HIREP	HOLD_FEM_HIREP	COHORT_B	SIZE_B	PO1_A	PO1_B	PO2_A	PO2_B	PO1_C	PO1_D	PO2_C	PO2_D
14102	C T	HELD_MAL_ADRCASE5UJLN	9	12	6	6	0	3	HELD_MAL_ADRCCTRL	56	72	40	21	30	5
14102	C T	HELD_FEM_HIRES	271	361	181	123	115	33	HELD_FEM_LORESP	281	340	222	107	126	48
14103	C T	HELD_FEM_HIRES	264	445	83	192	61	11	HELD_FEM_LORESP	273	482	64	209	64	0
14103	C T	HELD_FEM_VHIRES	137	234	40	103	28	6	HELD_FEM_VLORESP	135	236	34	101	34	0
14103	C T	HELD_FEM_UHIRES	53	84	22	35	14	4	HELD_FEM_ULORESP	69	121	17	52	17	0
14129	A G	HELD_ALL_ADRCASE3UJLN	47	53	41	18	17	12	HELD_ALL_ADRCCTRL	116	151	81	47	57	12
14129	A G	HELD_MAL_ADRCASE3UJLN	16	18	14	7	4	5	HELD_MAL_ADRCCTRL	55	72	38	22	28	5
14326	A C	HELD_FEM_HIRES	272	454	90	191	72	9	HELD_FEM_LORESP	285	449	121	181	87	17
14503	C T	HELD_ALL_ADRCASE5UJLN	24	34	14	16	2	6	HELD_ALL_ADRCCTRL	114	154	74	53	48	13
14503	C T	HELD_ALL_ADRCASE3UJLN	45	58	32	25	8	12	HELD_ALL_ADRCCTRL	114	154	74	53	48	13
14503	C T	HELD_FEM_ADRCASE5UJLN	16	21	11	10	1	5	HELD_FEM_ADRCCTRL	57	75	39	25	25	7
14503	C T	HELD_FEM_ADRCASE3UJLN	29	35	23	15	5	9	HELD_FEM_ADRCCTRL	57	75	39	25	25	7
14537	C T	HELD_ALL_ADRCASE	118	133	103	38	57	23	HELD_ALL_ADRCCTRL	113	156	70	52	52	9
14537	C T	HELD_FEM_ADRCASE	67	68	66	18	32	17	HELD_FEM_ADRCCTRL	59	76	42	22	32	5
15915	T C	HELD_FEM_ADRCASE	63	95	31	34	27	2	HELD_FEM_ADRCCTRL	55	80	30	35	10	10
15915	T C	HELD_ALL_ADRCASE	111	172	50	65	42	4	HELD_ALL_ADRCCTRL	106	158	54	67	24	15
15915	T C	HELD_ALL_ADRCASE3UJLN	38	66	10	29	8	1	HELD_ALL_ADRCCTRL	106	158	54	67	24	15
19289	G A	HELD_MAL_CASE	12	20	4	8	4	0	HELD_MAL_CTRL	18	34	2	17	0	1
19289	G A	HELD_ALL_CASE	43	71	15	28	15	0	HELD_ALL_CTRL	40	73	7	34	5	1
19289	G A	HELD_MAL_BAD	19	27	11	9	9	1	HELD_MAL_GOOD	34	59	9	25	.9	0
36958	C G	HELD_MAL_ADRCASE3UJLN	15	30	0	15	0	0	HELD_MAL_ADRCCTRL	57	104	10	47	10	0

BY5NR	A1	A2	COHORT_A	SIZE_A	FO1A	FO2A	FO1B	FO2B	COHORT_B	SIZE_B	FO1B	FO2B	FO1C	FO2C	FO1D	FO2D
37158	C	A	HELD_ALL_ADRCASE	122	139	105	40	59	23	HELD_ALL_ADRCTRL	114	157	71	53	51	10
37158	C	A	HELD_FEM_ADRCASE	66	70	62	18	34	14	HELD_FEM_ADRCTRL	58	77	39	23	31	4
37160	C	T	HELD_FEM_UHIRESP	53	86	20	36	14	3	HELD_FEM_ULORESP	73	133	13	60	13	0
37412	T	G	HELD_FEM_ADRCASE5ULN	17	19	15	3	13	1	HELD_FEM_ADRCTRL	69	98	40	35	28	6
37412	T	G	HELD_ALL_ADRCASE5ULN	26	32	20	7	18	1	HELD_ALL_ADRCTRL	129	185	73	65	55	9
37412	T	G	HELD_FEM_ADRCASE3ULN	31	35	27	10	15	6	HELD_FEM_ADRCTRL	69	98	40	35	28	6
37457	T	A	CVD_ALL_CASE	53	101	5	48	5	0	CVD_ALL_CTRL	28	43	13	18	7	3
37457	T	A	CVD_FEM_CASE	17	33	1	16	1	0	CVD_FEM_CTRL	18	27	9	11	5	2
37457	T	A	CVD_MAL_CASE	36	68	4	32	4	0	CVD_MAL_CTRL	10	16	4	7	2	1
37704	C	T	HELD_MAL_ADRCASE5ULN	9	17	1	8	1	0	HELD_MAL_ADRCTRL	60	120	0	60	0	0
38959	C	A	CVD_ALL_CASE	57	99	15	42	15	0	CVD_ALL_CTRL	31	55	7	26	3	2
38959	C	A	HELD_FEM_HIRESP	282	526	38	244	33	0	HELD_FEM_LORESP	280	508	52	232	44	4
39292	G	A	HELD_FEM_ADRCASE5ULN	9	12	6	5	2	2	HELD_FEM_ADRCTRL	47	82	12	36	10	1
39292	G	A	HELD_ALL_ADRCASE5ULN	17	26	8	11	4	2	HELD_ALL_ADRCTRL	86	153	19	70	13	3
39698	T	C	HELD_MAL_ADRCASE3ULN	16	13	19	1	11	4	HELD_MAL_ADRCTRL	56	60	52	19	22	15
39756	T	C	HELD_FEM_ADRCASE3ULN	19	29	9	13	3	3	HELD_FEM_ADRCTRL	44	51	37	19	13	12
39951	T	C	HELD_MAL_ADRCASE	52	78	26	26	26	0	HELD_MAL_ADRCTRL	54	72	36	26	20	8
39951	T	C	HELD_ALL_ADRCASE	117	161	73	48	65	4	HELD_ALL_ADRCTRL	113	159	67	59	41	13
39951	T	C	HELD_FEM_ADRCASE	65	83	47	22	39	4	HELD_FEM_ADRCTRL	59	87	31	33	21	5
39951	T	C	HELD_FEM_ADRCASE5ULN	14	15	13	3	9	2	HELD_FEM_ADRCTRL	59	87	31	33	21	5
40466	G	T	HELD_FEM_HIRESP	266	469	63	204	61	1	HELD_FEM_LORESP	266	436	96	183	70	13

STUDY	ALFA2	COHORT_A	SIZE_A	FOPA_A	FOPA_B	FOPA_C	FOPA_D	FOPA_E	COHORT_B	SIZE_B	FOT1_B	FOT2_B	FOT3_B	FOT4_B	FOT5_B	FOT6_B
40466	G T	HELD_FEM_UHRESP	52	93	11	41	11	0	HELD_FEM_ULORESP	69	110	28	47	16	6	
40466	G T	HELD_FEM_VHRESP	139	244	34	106	32	1	HELD_FEM_VLORESP	135	219	51	91	37	7	
44442	A G	HELD_MAL_ADRCASE5ULN	9	8	10	1	6	2	HELD_MAL_ADRCTRL	59	82	36	27	28	4	
55504	T C	HELD_MAL_ADRCASE	60	75	45	23	29	8	HELD_MAL_ADRCTRL	56	54	58	15	24	17	
55542	C A	HELD_FEM_ADRCASE	65	62	68	16	30	19	HELD_FEM_ADRCTRL	69	85	53	24	37	8	
55670	C T	HELD_FEM_VHRESP	154	297	11	143	11	0	HELD_FEM_VLORESP	138	254	22	116	22	0	
55736	A G	HELD_ALL_ADRCASE5ULN	15	30	0	15	0	0	HELD_ALL_ADRCTRL	87	147	27	62	23	2	
55736	A G	HELD_MAL_ADRCASE5ULN	7	14	0	7	0	0	HELD_MAL_ADRCTRL	43	71	15	28	15	0	
55736	A G	HELD_FEM_ADRCASE5ULN	8	16	0	8	0	0	HELD_FEM_ADRCTRL	44	76	12	34	8	2	
55748	T C	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	HELD_MAL_ADRCTRL	56	98	14	43	12	1	
55813	T C	HELD_ALL_ADRCASE3ULN	44	39	49	9	21	14	HELD_ALL_ADRCTRL	119	139	99	44	51	24	
55845	C A	HELD_FEM_VHRESP	136	152	120	40	72	24	HELD_FEM_VLORESP	135	179	91	61	57	17	
55845	C A	HELD_MAL_ADRCASE3ULN	16	25	7	9	7	0	HELD_MAL_ADRCTRL	58	68	48	18	32	8	
55845	C A	HELD_FEM_UHRESP	52	58	46	16	26	10	HELD_FEM_ULORESP	68	93	43	32	29	7	
55923	C T	HELD_FEM_ADRCASE	59	63	55	16	31	12	HELD_FEM_ADRCTRL	57	78	36	26	26	5	
55923	C T	HELD_FEM_ADRCASE3ULN	27	27	27	7	13	7	HELD_FEM_ADRCTRL	57	78	36	26	26	5	
55945	G A	HELD_FEM_ADRCASE	66	70	62	18	34	14	HELD_FEM_ADRCTRL	65	92	38	32	28	5	
55945	G A	HELD_FEM_ADRCASE3ULN	28	29	27	8	13	7	HELD_FEM_ADRCTRL	65	92	38	32	28	5	
55945	G A	HELD_ALL_ADRCASE	124	142	106	43	56	25	HELD_ALL_ADRCTRL	122	163	81	54	55	13	
56007	T C	HELD_MAL_ADRCASE3ULN	17	26	8	13	0	4	HELD_MAL_ADRCTRL	49	63	35	24	15	10	
56007	T C	HELD_MAL_ADRCASE5ULN	9	14	4	7	0	2	HELD_MAL_ADRCTRL	49	63	35	24	15	10	

INVSNP	AI A2	COHORT_A	SIZE_A	FO1A	FO2A	FO11	FO12	FO22	COHORT_B	SIZE_B	FO1B	FO2B	FO1L	FO2L	FO22
56011	A	G	HELD_ALL_ADRCASE5ULN	24	48	0	24	0	0	0	228	12	108	12	0
56104	G	A	HELD_FEM_UHRESP	56	62	50	18	26	12	76	106	46	34	38	4
56113	G	T	HELD_ALL_ADRCASE5ULN	24	20	28	7	6	11	114	133	95	41	51	22
56113	G	T	HELD_ALL_ADRCASE5ULN	45	47	43	18	11	16	114	133	95	41	51	22
56113	G	T	HELD_FEM_ADRCASE5ULN	17	13	21	4	5	8	58	68	48	20	28	10
56113	G	T	HELD_FEM_ADRCASE3ULN	30	28	32	10	8	12	58	68	48	20	28	10
56636	T	C	HELD_FEM_ADRCASE	70	72	68	23	26	21	59	65	53	14	37	8
56636	T	C	HELD_FEM_ADRCASE3ULN	31	36	26	13	10	8	59	65	53	14	37	8
56636	T	C	HELD_FEM_ADRCASE5ULN	18	19	17	7	5	6	59	65	53	14	37	8
56666	G	A	HELD_MAL_ADRCASE3ULN	13	0	26	13	0	0	55	89	21	44	1	10
56666	G	A	HELD_MAL_ADRCASE5ULN	8	0	16	8	0	0	55	89	21	44	1	10
56666	G	A	HELD_MAL_ADRCASE	51	94	8	47	0	4	55	89	21	44	1	10
56667	T	C	HELD_FEM_UHRESP	264	342	186	108	126	30	265	304	226	88	128	49
56667	T	C	HELD_MAL_ADRCASE3ULN	17	28	6	14	0	3	56	71	41	35	1	20
56667	T	C	HELD_FEM_ADRCASE3ULN	30	29	31	6	17	7	67	85	49	27	31	9
56780	G	A	HELD_FEM_ADRCASE3ULN	26	19	33	1	17	8	50	58	42	14	30	6
56780	G	A	HELD_FEM_ADRCASE	62	51	73	9	33	20	50	58	42	14	30	6
56780	G	A	HELD_ALL_ADRCASE3ULN	36	28	44	3	22	11	94	105	83	26	53	15
56780	G	A	HELD_ALL_ADRCASE	105	96	114	21	54	30	94	105	83	26	53	15
56876	T	C	HELD_FEM_UHRESP	57	106	8	50	6	1	74	123	25	51	21	2
56876	T	C	HELD_FEM_UHRESP	285	524	46	243	38	4	274	480	68	211	58	5

SNP	AI A2	COHORT_A	SIZE_A	FOI_A	FOR_A	FOI2_A	FOR2_A	COHORT_B	SIZE_B	FOI_B	FOR2_B	FOR1_B	FOI2_B	TO2_B	
56876	T C	HELD_FEM_VHRESP	154	285	23	132	21	1	HELD_FEM_VLORESP	143	248	38	108	32	3
56978	A G	HELD_ALL_ADRCASE5ULN	26	42	10	17	8	1	HELD_ALL_ADRCTRL	124	157	91	53	51	20
57000	A T	HELD_FEM_VHRESP	150	206	94	68	70	12	HELD_FEM_VLORESP	143	206	80	81	44	18
57000	A T	HELD_FEM_UHRESP	54	76	32	25	26	3	HELD_FEM_ULORESP	75	104	46	41	22	12
57000	A T	CVD_ALL_CASE	57	91	23	35	21	1	CVD_ALL_CTRL	32	43	21	16	11	5
57000	A T	CVD_MAL_CASE	39	64	14	25	14	0	CVD_MAL_CTRL	13	18	8	7	4	2
57313	T C	HELD_FEM_UHRESP	55	65	45	23	19	13	HELD_FEM_ULORESP	76	104	48	34	36	6
57734	C G	HELD_FEM_ADRCASE3ULN	30	45	15	17	11	2	HELD_FEM_ADRCTRL	67	116	18	51	14	2
57837	A G	HELD_MAL_ADRCASE3ULN	15	28	2	13	2	0	HELD_MAL_ADRCTRL	53	83	23	33	17	3
57853	T C	HELD_FEM_HRESP	265	457	73	194	69	2	HELD_FEM_LORESP	265	425	105	176	73	16
57853	T C	HELD_FEM_UHRESP	52	91	13	39	13	0	HELD_FEM_ULORESP	68	104	32	43	18	7
57853	T C	HELD_FEM_VHRESP	139	238	40	100	38	1	HELD_FEM_VLORESP	135	214	56	87	40	8
57854	G A	HELD_FEM_HRESP	267	451	83	187	77	3	HELD_FEM_LORESP	262	420	104	172	76	14
57854	G A	HELD_FEM_UHRESP	52	90	14	38	14	0	HELD_FEM_ULORESP	68	104	32	42	20	6
57854	G A	HELD_MAL_ADRCASE3ULN	16	29	3	13	3	0	HELD_MAL_ADRCTRL	57	86	28	33	20	4
58295	A G	HELD_MAL_ADRCASE	56	48	64	13	22	21	HELD_MAL_ADRCTRL	54	60	48	14	32	8
58402	T C	HELD_MAL_ADRCASE3ULN	17	10	24	5	0	12	HELD_MAL_ADRCTRL	56	57	55	28	1	27
58407	G T	HELD_FEM_VHRESP	153	195	111	59	77	17	HELD_FEM_VLORESP	145	180	110	65	50	30
58407	G T	HELD_FEM_UHRESP	56	76	36	23	30	3	HELD_FEM_ULORESP	76	91	61	31	29	16
58440	T C	HELD_FEM_UHRESP	52	81	23	32	17	3	HELD_FEM_ULORESP	72	127	17	56	15	1
58525	C T	HELD_FEM_ADRCASE	66	110	22	47	16	3	HELD_FEM_ADRCTRL	66	128	4	63	2	1

BASENP	AI A2	COHORT_A	SIZE_A	FO1_A	FO2_A	FO11_A	FO12_A	FO22_A	COHORT_B	SIZE_B	FO1_B	FO2_B	FO11_B	FO12_B	FO22_B
58525	C T	HELD_FEM_ADRCASE3ULN	30	49	11	20	9	1	HELD_FEM_ADRCTRL	66	128	4	63	2	1
58525	C T	HELD_FEM_ADRCASE3ULN	16	26	6	10	6	0	HELD_FEM_ADRCTRL	66	128	4	63	2	1
58525	C T	HELD_ALL_ADRCASE	124	212	36	94	24	6	HELD_ALL_ADRCTRL	122	228	16	108	12	2
58525	C T	HELD_ALL_ADRCASE3ULN	25	42	8	17	3	0	HELD_ALL_ADRCTRL	122	228	16	108	12	2
58525	C T	HELD_ALL_ADRCASE3ULN	47	80	14	34	12	1	HELD_ALL_ADRCTRL	122	228	16	108	12	2
58533	C T	HELD_FEM_ADRCASE	67	114	20	50	14	3	HELD_FEM_ADRCTRL	71	136	6	66	4	1
58533	C T	HELD_FEM_ADRCASE3ULN	27	46	8	20	6	1	HELD_FEM_ADRCTRL	71	136	6	66	4	1
58533	C T	HELD_FEM_ADRCASE3ULN	14	24	4	10	4	0	HELD_FEM_ADRCTRL	71	136	6	66	4	1
58533	C T	HELD_ALL_ADRCASE	125	217	33	98	21	6	HELD_ALL_ADRCTRL	129	238	20	112	14	3
58544	G A	HELD_MAL_ADRCASE3ULN	6	0	12	6	0	0	HELD_MAL_ADRCTRL	54	85	23	35	15	4
58716	T C	HELD_MAL_ADRCASE3ULN	16	30	2	15	0	1	HELD_MAL_ADRCTRL	59	76	42	38	0	21
58716	T C	HELD_MAL_ADRCASE3ULN	8	14	2	7	0	1	HELD_MAL_ADRCTRL	59	76	42	38	0	21
58736	C T	HELD_FEM_HIRES	289	395	183	139	117	33	HELD_FEM_LORESP	281	344	218	106	132	43
58808	A G	HELD_FEM_ADRCASE	68	100	36	38	24	6	HELD_FEM_ADRCTRL	61	74	48	22	30	9
58809	C A	HELD_MAL_ADRCASE3ULN	9	0	18	9	0	0	HELD_MAL_ADRCTRL	59	96	22	40	16	3
58809	C A	HELD_ALL_ADRCASE3ULN	46	70	22	31	8	7	HELD_ALL_ADRCTRL	128	215	41	91	33	4
58809	C A	HELD_MAL_ADRCASE3ULN	16	23	9	11	1	4	HELD_MAL_ADRCTRL	59	96	22	40	16	3
58809	C A	HELD_FEM_HIRES	54	94	14	40	14	0	HELD_FEM_ULORESP	75	116	34	44	28	3
58886	A G	HELD_FEM_ADRCASE3ULN	31	20	42	3	14	14	HELD_FEM_ADRCTRL	72	74	70	19	36	17
58886	A G	HELD_ALL_ADRCASE3ULN	48	38	58	7	24	17	HELD_ALL_ADRCTRL	132	142	122	39	64	29
58886	A G	HELD_ALL_ADRCASE3ULN	26	20	32	3	14	9	HELD_ALL_ADRCTRL	132	142	122	39	64	29

BASE NP	M1 A2	COHORT_A	SIZE	FO1	FO2	FO11	FO12	FO22	COHORT_B	SIZE	FO1-B	FO2-B	FO1H	FO2H	FO22
58926	C T	HELD_MAL_ADRCASE5ULN	15	12	18	2	8	5	HELD_MAL_ADRCTRL	54	75	33	27	21	6
58926	C T	HELD_ALL_ADRCASE5ULN	22	19	25	4	11	7	HELD_ALL_ADRCTRL	113	144	82	48	48	17
58926	C T	CVD_FEM_CASE	18	21	15	8	5	5	CVD_FEM_CTRL	19	21	17	4	13	2
58926	C T	HELD_MAL_ADRCASE5ULN	8	7	9	1	5	2	HELD_MAL_ADRCTRL	54	75	33	27	21	6
58968	A G	HELD_ALL_ADRCASE5ULN	22	21	23	6	9	7	HELD_ALL_ADRCTRL	118	168	68	70	28	20
58968	A G	HELD_MAL_ADRCASE5ULN	13	12	14	3	6	4	HELD_MAL_ADRCTRL	55	81	29	34	13	8
58968	A G	HELD_ALL_ADRCASE5ULN	41	47	35	17	13	11	HELD_ALL_ADRCTRL	118	168	68	70	28	20
58968	A G	HELD_FEM_ADRCASE5ULN	14	13	15	4	5	5	HELD_FEM_ADRCTRL	63	87	39	36	15	12
58985	G A	HELD_ALL_ADRCASE5ULN	26	28	24	8	12	6	HELD_ALL_ADRCTRL	130	188	72	69	50	11
59113	C G	HELD_MAL_ADRCASE5ULN	8	2	14	1	0	7	HELD_MAL_ADRCTRL	55	64	46	32	0	23
59113	C G	HELD_MAL_ADRCASE5ULN	16	10	22	5	0	11	HELD_MAL_ADRCTRL	55	64	46	32	0	23
59236	G A	HELD_ALL_ADRCASE5ULN	95	103	87	34	35	26	HELD_ALL_ADRCTRL	96	122	70	37	48	11
59236	G A	HELD_ALL_ADRCASE5ULN	34	39	29	15	9	10	HELD_ALL_ADRCTRL	96	122	70	37	48	11
59236	G A	HELD_FEM_ADRCASE5ULN	52	47	57	15	17	20	HELD_FEM_ADRCTRL	51	59	43	16	27	8
59237	C T	HELD_FEM_VHRESP	121	140	102	36	68	17	HELD_FEM_VLORESP	119	138	100	46	46	27
59237	C T	HELD_FEM_HRESP	240	290	190	84	122	34	HELD_FEM_LORESP	243	285	201	94	97	52
59267	T C	HELD_FEM_UHRESP	50	52	48	17	18	15	HELD_FEM_ULORESP	68	96	40	31	34	3
59352	T C	HELD_MAL_ADRCASE	58	73	43	18	37	3	HELD_MAL_ADRCTRL	56	74	38	26	22	8
59352	T C	HELD_ALL_ADRCASE	126	167	85	48	71	7	HELD_ALL_ADRCTRL	125	164	86	55	54	16
59363	T C	CVD_MAL_CASE	60	84	36	31	22	7	CVD_MAL_CTRL	28	30	26	11	8	9
59368	T C	HELD_FEM_ADRCASE	66	74	58	23	28	15	HELD_FEM_ADRCTRL	69	100	38	35	30	4

SNP	A1	A2	COHORT_A	SIZE	F01_A	F02_A	F01_B	F02_B	COHORT_B	SIZE	F01_B	F02_B	F01_C	F02_C
59371	C	T	HELD_FEM_VHRESP	141	153	129	48	57	36	136	164	108	43	78
59371	C	T	HELD_FEM_UHRESP	52	60	44	22	16	14	68	88	48	26	36
59372	C	T	HELD_MAL_ADRCASE	55	87	23	38	11	6	58	104	12	48	8
59372	C	T	HELD_MAL_ADRCASEULN	17	26	8	11	4	2	58	104	12	48	8
59443	T	C	HELD_ALL_ADRCASE5ULN	19	25	13	11	3	5	95	110	80	27	56
59443	T	C	HELD_MAL_ADRCASE5ULN	7	7	7	3	1	3	45	47	43	9	29
900080	G	C	HELD_FEM_ADRCASE3ULN	31	52	10	22	3	1	71	135	7	65	5
900080	G	C	HELD_FEM_ADRCASE5ULN	17	29	5	12	5	0	71	135	7	65	5
900102	T	G	HELD_FEM_UHRESP	55	73	37	26	21	8	78	76	80	17	42
900102	T	G	HELD_FEM_VHRESP	153	204	102	69	66	18	147	168	126	46	76
900111	G	A	HELD_FEM_UHRESP	55	73	37	26	21	8	78	79	77	19	41
900111	G	A	HELD_FEM_VHRESP	151	198	104	66	66	19	146	166	126	44	78
900117	T	G	HELD_MAL_BAD	17	31	3	14	3	0	33	44	22	16	12
900118	G	A	HELD_FEM_HIRESF	252	469	35	219	31	2	259	444	74	193	58
900118	G	A	HELD_FEM_VHRESP	130	241	19	113	15	2	130	225	35	100	25
900118	G	A	HELD_FEM_ADRCASE5ULN	15	28	2	14	0	1	59	109	9	50	9
900118	G	A	HELD_ALL_ADRCASE5ULN	23	42	4	21	0	2	110	205	15	97	11
900120	T	C	HELD_FEM_HIRESF	286	511	61	228	55	3	280	471	89	206	59
900121	T	G	HELD_FEM_HIRESF	269	353	185	120	113	36	266	379	153	134	111
900123	A	G	HELD_ALL_ADRCASE	119	238	0	119	0	0	115	226	4	111	4
900123	A	G	HELD_FEM_ADRCASE	64	128	0	64	0	0	59	115	3	56	3

DAVSNP	AT/AZ	COHORT_A	SIZE_A	FOZ_A	FOZ_B	FOZ_C	FOZ_D	FOZ_E	COHORT_B	SIZE_B	FOZ_B	FOZ_C	FOZ_D	FOZ_E	FOZ_F	FOZ_G	FOZ_H	FOZ_I	FOZ_J	FOZ_K	FOZ_L	FOZ_M	FOZ_N	FOZ_O	FOZ_P	FOZ_Q	FOZ_R	FOZ_S	FOZ_T	FOZ_U	FOZ_V	FOZ_W	FOZ_X	FOZ_Y	FOZ_Z	
900124	G A	HELD_FEM_HIRBSP	249	254	244	31	192	26	HELD_FEM_LORESP	253	288	218	55	178	20																					
900132	T C	HELD_FEM_ADRCASE	67	111	23	44	23	0	HELD_FEM_ADRCTRL	58	89	27	37	15	6																					
900144	A G	CVD_FEM_CASE	28	56	0	28	0	0	CVD_FEM_CTRL	40	74	6	34	6	0																					
900144	A G	HELD_ALL_ADRCASE5ULN	26	52	0	26	0	0	HELD_ALL_ADRCTRL	125	240	10	115	10	0																					
900145	G T	CVD_FEM_CASE	30	58	2	29	0	1	CVD_FEM_CTRL	39	73	5	34	5	0																					
900145	G T	HELD_ALL_ADRCASE5ULN	25	50	0	25	0	0	HELD_ALL_ADRCTRL	121	232	10	111	10	0																					
900146	A G	HELD_FEM_ADRCASE5ULN	17	22	12	7	8	2	HELD_FEM_ADRCTRL	67	109	25	42	25	0																					
900146	A G	HELD_FEM_CASE	30	50	10	20	10	0	HELD_FEM_CTRL	22	34	10	15	4	3																					
900146	A G	HELD_MAL_ADRCASE	58	97	19	39	19	0	HELD_MAL_ADRCTRL	54	84	24	34	16	4																					
900147	T C	HELD_ALL_ADRCASE5ULN	44	74	14	31	12	1	HELD_ALL_ADRCTRL	119	168	70	61	46	12																					
900147	T C	HELD_FEM_ADRCASE5ULN	28	48	8	21	6	1	HELD_FEM_ADRCTRL	66	91	41	31	29	6																					
900196	C T	HELD_MAL_BAD	19	17	21	5	7	7	HELD_MAL_GOOD	32	47	17	20	7	5																					
900196	C T	HELD_FEM_BAD	12	19	5	8	3	1	HELD_FEM_GOOD	36	37	35	8	21	7																					
900196	C T	HELD_FEM_ADRCASE5ULN	23	37	9	14	9	0	HELD_FEM_ADRCTRL	62	77	47	24	29	9																					
900196	C T	CVD_FEM_CASE	6	8	4	2	4	0	CVD_FEM_CTRL	15	20	10	9	2	4																					
900196	C T	CVD_ALL_CASE	21	30	12	10	10	1	CVD_ALL_CTRL	31	36	26	14	8	9																					
900200	T C	CVD_FEM_CASE	20	23	17	6	11	3	CVD_FEM_CTRL	38	58	18	23	12	3																					
900204	C G	HELD_FEM_HIRBSP	270	430	110	160	110	0	HELD_FEM_LORESP	261	384	138	123	138	0																					
900205	C G	HELD_FEM_HIRBSP	283	364	202	111	142	30	HELD_FEM_LORESP	274	380	168	138	104	32																					
900205	C G	CVD_MAL_CASE	69	90	48	29	32	8	CVD_MAL_CTRL	31	49	13	18	13	0																					
900223	G A	HELD_FEM_ADRCASE	43	85	1	42	1	0	HELD_FEM_ADRCTRL	31	57	5	27	3	1																					

BR/STP	A1/A2	COHORT_A	SIZE_A	FO_A	FO2_A	FO1_A	FO12_A	FO22_A	COHORT_B	SIZE_B	FO1_B	FO2_B	FO12_B	FO22_B
900225	G A	HELD_ALL_ADRCASESULN	23	0	46	23	0	0	HELD_ALL_ADRCTRL	126	234	18	108	0
900225	G A	HELD_MAL_ADRCASESULN	15	0	30	15	0	0	HELD_MAL_ADRCTRL	57	104	10	47	0
900227	A C	HELD_FEM_ADRCASESULN	17	33	1	16	1	0	HELD_FEM_ADRCTRL	72	118	26	48	2
900233	T A	HELD_FEM_ADRCASESULN	17	23	11	10	3	4	HELD_FEM_ADRCTRL	72	84	60	23	11
900236	C T	HELD_FEM_ADRCASESULN	31	50	12	19	12	0	HELD_FEM_ADRCTRL	69	125	13	57	1
900236	C T	HELD_MAL_ADRCASESULN	9	18	0	9	0	0	HELD_MAL_ADRCTRL	60	104	16	45	1
900241	C G	HELD_FEM_HIRES	276	367	185	134	99	43	HELD_FEM_LORESP	275	373	177	124	26
900242	G C	HELD_ALL_ADRCASESULN	26	0	52	26	0	0	HELD_ALL_ADRCTRL	132	220	44	99	11
900242	G C	HELD_ALL_ADRCASESULN	48	93	3	45	3	0	HELD_ALL_ADRCTRL	132	220	44	99	11
900242	G C	HELD_FEM_ADRCASESULN	17	0	34	17	0	0	HELD_FEM_ADRCTRL	72	119	25	49	2
900242	G C	HELD_MAL_ADRCASESULN	17	0	34	17	0	0	HELD_MAL_ADRCTRL	60	101	19	50	1
900242	G C	HELD_FEM_ADRCASE	73	136	10	63	10	0	HELD_FEM_ADRCTRL	72	119	25	49	2
900242	G C	HELD_FEM_ADRCASESULN	31	59	3	28	3	0	HELD_FEM_ADRCTRL	72	119	25	49	2
900242	G C	HELD_ALL_ADRCASE	136	246	26	118	10	8	HELD_ALL_ADRCTRL	132	220	44	99	11
900242	G C	HELD_MAL_ADRCASESULN	9	0	18	9	0	0	HELD_MAL_ADRCTRL	60	101	19	50	1
900242	G C	HELD_MAL_ADRCASESULN	9	0	18	9	0	0	HELD_MAL_ADRCTRL	60	101	19	50	1

Table 5b p-values of PA SNPs

A SNP is considered as associated to cardiovascular disease, adverse statin response or to efficacy of statin treatment, respectively, when one of the p values is equal or below 0.05.

BAVSNP	COMPARISON	GTTYPE CPVAL	GTTYPE XPVAL	GTTYPE ERPVAL	ALLELE CEVAL	ALLELE XPVAL	ALLELE ERPVAL
29	HELD_FEM_LIP	0,0996	0,0983	0,0976	0,0441	0,0533	0,0438
29	HELD_ALL_ADR3ULN	0,0483	0,0484	0,0493	0,1053	0,1185	0,1048
29	HELD_ALL_LIP	0,0912	0,0952	0,091	0,0503	0,0625	0,05
52	HELD_ALL_CC	0,0112	0,0128	0,0099	0,0015	0,0023	0,0014
52	HELD_MAL_HDL	0,0237	0,0238	0,0194	0,8213	0,8292	0,8214
52	HELD_FEM_CC	0,0818	0,0956	0,08	0,0293	0,0436	0,0282
52	HELD_MAL_CC	0,1499	0,2053	0,1393	0,0303	0,0547	0,0298
52	HELD_MAL_LIP2	0,1121	0,1133	0,1112	0,0423	0,0429	0,0422
57	HELD_FEM_CC	0,0168	0,008	0,0108	0,0076	0,0106	0,0049
118	HELD_MAL_LIP2	0,1081	0,1089	0,1043	0,0466	0,0501	0,0462
137	HELD_MAL_ADR5ULN	0,0575	0,0872	0,0156	0,0892	0,1027	0,0951
137	HELD_ALL_ADR5ULN	0,0307	0,0274	0,0218	0,2446	0,2504	0,2486
137	HELD_ALL_ADR3ULN	0,034	0,035	0,0255	0,0671	0,0747	0,0686
179	HELD_MAL_ADR5ULN	0,0094	0,0241	0,0154	0,9216	1	0,921
179	HELD_MAL_ADR3ULN	0,0452	0,0479	0,0408	0,5445	0,7636	0,5327
179	HELD_ALL_ADR5ULN	0,0415	0,0537	0,0756	0,7311	0,8135	0,7272
179	HELD_ALL_ADR	0,0691	0,0447	0,0464	0,2487	0,3013	0,2482
240	HELD_ALL_ADR3ULN	0,1154	0,1318	0,0756	0,04	0,0539	0,0281
240	HELD_MAL_ADR3ULN	0,0641	0,0976	0,0399	0,0835	0,1215	0,0507
241	HELD_ALL_ADR3ULN	0,0987	0,0984	0,1033	0,0237	0,0301	0,0262
241	HELD_ALL_ADR5ULN	0,1495	0,1519	0,1611	0,04	0,0527	0,0464
241	HELD_MAL_ADR3ULN	0,1757	0,2127	0,1775	0,0411	0,055	0,0459
288	CVD_ALL	0,1013	0,1098	0,0863	0,0462	0,0557	0,0441
384	CVD_ALL	0,0214	0,022	0,0205	0,1828	0,1946	0,1831
384	HELD_FEM_CC	0,0793	0,0887	0,0704	0,0214	0,0299	0,021
533	CVD_ALL	0,0955	0,0932	0,0905	0,0387	0,0482	0,0359
542	HELD_FEM_ADR	0,0522	0,0292	0,0417	0,0922	0,1056	0,0907

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BAVSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
576	HELD_ALL_LIP	0,0349	0,0626	0,0117	0,036	0,0641	0,012
576	HELD_FEM_LIP	0,0403	0,0571	0,0165	0,0416	0,0583	0,017
608	CVD_MAL	0,0031	0,0027	0,002	0,0027	0,0035	0,0035
614	HELD_MAL_HDL	0,0069	0,0113	0,0025	0,0001	0,0001	0
614	HELD_ALL_CC	0,0045	0,0037	0,0031	0,0052	0,008	0,0047
614	HELD_MAL_CC	0,0694	0,1277	0,0689	0,0102	0,0154	0,0101
614	HELD_MAL_LIP	0,1792	0,254	0,1858	0,0113	0,0153	0,0123
614	CVD_ALL	0,1654	0,1652	0,1594	0,0202	0,0237	0,0188
614	HELD_FEM_CC	0,031	0,0198	0,0239	0,0446	0,0537	0,0387
738	CVD_ALL	0,0999	0,1019	0,0962	0,0261	0,0303	0,0257
1056	HELD_ALL_HDL	0,1007	0,1082	0,0989	0,0323	0,0468	0,0304
1056	HELD_FEM_LIP	0,0488	0,0518	0,0403	0,0695	0,09	0,0691
1092	HELD_MAL_ADR5ULN	0,0404	0,0443	0,0114	0,6514	0,7766	0,6465
1524	HELD_MAL_CC2	0,0122	0,0142	0,0107	0,0079	0,0113	0,0062
1524	HELD_ALL_LIP	0,0507	0,0381	0,0237	0,0592	0,0717	0,0581
1524	HELD_ALL_CC	0,0681	0,0671	0,0561	0,025	0,0318	0,0248
1574	CVD_MAL	0,0611	0,0678	0,0422	0,3189	0,4133	0,3254
1582	HELD_MAL_ADR3ULN	0,1522	0,1512	0,0956	0,0468	0,0648	0,0295
1657	HELD_FEM_EFF	0,05	0,0604	0,047	0,4599	0,5588	0,459
1722	CVD_MAL	0,013	0,0128	0,0135	0,3717	0,4376	0,3729
1756	HELD_MAL_ADR5ULN	0,0321	0,0857	0,1003	0,0402	0,063	0,068
1757	HELD_ALL_CC	0,02	0,0205	0,0053	0,3618	0,386	0,3603
1757	HELD_FEM_CC	0,0517	0,0569	0,015	0,1242	0,1342	0,1193
1757	HELD_FEM_VEFF	0,1217	0,1247	0,1208	0,0423	0,0505	0,0422
1757	HELD_MAL_ADR	0,0536	0,05	0,0501	0,6703	0,7693	0,6702
1765	HELD_ALL_LIP	0,0466	0,0494	0,0442	0,3068	0,3533	0,3058
1767	HELD_ALL_ADR3ULN	0,0082	0,0075	0,0036	0,0053	0,0066	0,0026
1767	HELD_ALL_ADR5ULN	0,0608	0,0467	0,0302	0,0196	0,0231	0,0086
1767	HELD_MAL_ADR5ULN	0,183	0,216	0,0679	0,075	0,1229	0,0194
1767	HELD_FEM_ADR3ULN	0,0371	0,0348	0,0221	0,0341	0,0408	0,0251
1767	HELD_MAL_ADR3ULN	0,1692	0,1875	0,1061	0,0606	0,0741	0,0334
1837	HELD_ALL_ADR3ULN	0,0408	0,0398	0,0402	0,0225	0,0282	0,0196

DBAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
1837	HELD_FEM_LIP	0,0337	0,0356	0,0328	0,3132	0,3242	0,3131
1837	HELD_ALL_LIP	0,0466	0,046	0,0452	0,3884	0,3987	0,3879
1837	HELD_ALL_ADR	0,052	0,0488	0,0514	0,0709	0,075	0,0708
1854	HELD_FEM_LIP	0,0512	0,0527	0,05	0,0661	0,07	0,0658
1862	HELD_FEM_LIP	0,0562	0,058	0,0534	0,0231	0,0264	0,0229
2085	HELD_FEM_CC	0,0149	0,0109	0,0118	0,0081	0,0096	0,0081
2085	HELD_ALL_CC	0,0388	0,038	0,0345	0,0185	0,02	0,0183
2093	HELD_MAL_CC	0,047	0,0249	0,037	0,0015	0,002	0,0013
2093	HELD_ALL_CC	0,1596	0,1532	0,1414	0,04	0,0501	0,0383
2109	HELD_MAL_HDL	0,0044	0,0028	0,0023	0,0341	0,0543	0,0299
2109	HELD_ALL_HDL	0,0187	0,0127	0,0131	0,059	0,065	0,0546
2109	HELD_ALL_LIP2	0,0438	0,0439	0,0434	0,015	0,0152	0,0148
2109	HELD_FEM_LIP	0,0612	0,0563	0,059	0,0214	0,0277	0,0209
2124	HELD_MAL_LIP	0,1532	0,2284	0,153	0,0434	0,0557	0,0433
2140	HELD_FEM_UEFF	0,0437	0,0427	0,0203	0,009	0,0116	0,0069
2140	HELD_FEM_EFF	0,0174	0,0167	0,0136	0,0082	0,009	0,008
2140	HELD_MAL_ADR	0,0596	0,0738	0,0227	0,0301	0,0429	0,0285
2140	HELD_FEM_VEFF	0,0915	0,0872	0,0888	0,0284	0,0379	0,0277
2141	HELD_MAL_ADR3ULN	0,0844	0,0968	0,0461	0,0218	0,0238	0,0116
2141	HELD_FEM_UEFF	0,0776	0,0859	0,0221	0,1372	0,1469	0,1323
2141	HELD_MAL_ADR	0,0548	0,0515	0,0254	0,0347	0,0399	0,0344
2186	HELD_MAL_ADR5ULN	0,0287	0,0843	0,1009	0,0498	0,0718	0,0798
2187	HELD_FEM_ADR3ULN	0,0517	0,0567	0,0507	0,0495	0,0613	0,0529
2192	HELD_FEM_ADR	0,0008	0,0011	0,0003	0,0011	0,0014	0,0004
2192	HELD_FEM_ADR3ULN	0,0114	0,0187	0,0015	0,0146	0,0232	0,0019
2192	HELD_ALL_ADR	0,0234	0,0113	0,0173	0,0053	0,0068	0,0044
2192	HELD_FEM_ADR5ULN	0,0613	0,1149	0,0155	0,073	0,1305	0,0181
2192	HELD_ALL_ADR3ULN	0,1807	0,1865	0,1212	0,0607	0,0756	0,039
2203	HELD_FEM_LIP	0,0132	0,011	0,0126	0,0101	0,0118	0,0098
2203	HELD_ALL_LIP	0,0296	0,0294	0,029	0,042	0,0442	0,0422
2217	HELD_MAL_CC	0,0089	0,0048	0,0053	0,0074	0,0101	0,0071
2217	CVD_FEM	0,1624	0,1741	0,1076	0,0384	0,0539	0,0314

BAYSNP	COMPARISON	CTYPE CPVAL	CTYPE XPVAL	CTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
2281	HELD_FEM_CC	0,0422	0,0439	0,0393	0,0076	0,0102	0,0072
2281	HELD_MAL_CC	0,0529	0,0593	0,0174	0,0834	0,1238	0,0807
2284	HELD_MAL_LIP	0,0754	0,0848	0,0464	0,0227	0,0292	0,0137
2290	HELD_MAL_CC	0,0301	0,0636	0,0267	0,0022	0,0031	0,0017
2327	HELD_MAL_ADR	0,0279	0,0298	0,0262	0,0923	0,1092	0,092
2327	HELD_MAL_ADR5ULN	0,047	0,0358	0,0381	0,3085	0,4458	0,3068
2327	HELD_MAL_ADR3ULN	0,0396	0,0397	0,0429	0,0919	0,116	0,0897
2327	HELD_FEM_EFF	0,0462	0,0457	0,0458	0,0998	0,1039	0,0998
2353	CVD_MAL	0,0703	0,0407	0,0139	0,0223	0,0233	0,0031
2353	HELD_ALL_CC	0,0255	0,0122	0,0224	0,0659	0,0929	0,0654
2353	CVD_ALL	0,1352	0,1146	0,0973	0,0468	0,0506	0,0347
2353	HELD_FEM_CC	0,0743	0,0491	0,0628	0,1836	0,3092	0,1885
2371	HELD_ALL_LIP2	0,018	0,018	0,0181	0,043	0,0444	0,0432
2376	HELD_ALL_LIP2	0,03	0,038	0,0302	0,0327	0,0411	0,0329
2401	HELD_FEM_UEFF	0,0263	0,0256	0,0266	0,1128	0,1233	0,1146
2463	HELD_ALL_CC	0,0122	0,0147	0,0028	0,0144	0,0168	0,0033
2463	HELD_FEM_CC	0,0257	0,0328	0,0074	0,0307	0,0376	0,0088
2463	HELD_FEM_LIP2	0,0915	0,0988	0,0431	0,7177	0,7419	0,718
2755	HELD_FEM_ADR	0,0203	0,0192	0,0178	0,0222	0,024	0,022
2755	HELD_ALL_ADR	0,0325	0,035	0,03	0,0499	0,0513	0,0496
2755	HELD_FEM_EFF	0,0455	0,0449	0,0446	0,4065	0,4262	0,4065
2925	HELD_FEM_VEFF	0,0168	0,0169	0,0162	0,0055	0,0058	0,0055
2925	HELD_FEM_UEFF	0,0184	0,0176	0,0181	0,009	0,0119	0,0088
3043	HELD_FEM_ADR3ULN	0,031	0,0498	0,0233	0,0515	0,0764	0,0376
3152	HELD_FEM_VEFF	0,0204	0,0206	0,0196	0,3254	0,333	0,3253
3214	HELD_FEM_VEFF	0,0379	0,0331	0,0261	0,4369	0,4475	0,437
3215	HELD_MAL_ADR5ULN	0,0093	0,1304	0,041	0,0096	0,1304	0,0423
3237	HELD_FEM_CC	0,0174	0,0276	0,0167	0,0218	0,0323	0,0211
3241	HELD_MAL_ADR	0,111	0,1115	0,1048	0,0334	0,0418	0,033
3826	HELD_MAL_ADR5ULN	0,2155	0,1993	0,0862	0,0716	0,1186	0,0187
3826	HELD_ALL_ADR5ULN	0,254	0,2956	0,1522	0,0707	0,0873	0,038
3826	HELD_MAL_ADR3ULN	0,2528	0,2755	0,1635	0,0732	0,1143	0,044

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BAYENP	COMPARISON	CTTYPE	CTTYPE	CTTYPE	ALLELE	ALLELE	ALLELE
		CPVAL	XPVAL	LRPVAL	CPVAL	XPVAL	LRPVAL
3842	CVD_ALL	0,0096	0,0142	0,0014	0,0108	0,0157	0,0016
3842	CVD_MAL	0,0682	0,0966	0,0207	0,0735	0,1027	0,0222
3842	CVD_FEM	0,0717	0,1136	0,0359	0,0751	0,1165	0,0376
3843	HELD_MAL_CC2	0,0207	0,0236	0,0084	0,0758	0,1046	0,0759
3843	HELD_FEM_HDL	0,0447	0,024	0,0146	0,1239	0,1687	0,1233
3869	HELD_FEM_UEFF	0,0491	0,0538	0,0488	0,0211	0,0244	0,0202
3942	HELD_FEM_UEFF	0,0206	0,0152	0,0122	0,0028	0,0041	0,0029
4018	HELD_MAL_LIP	0,1128	0,1214	0,0532	0,037	0,0451	0,0313
4206	HELD_ALL_ADR3ULN	0,1055	0,1128	0,1103	0,041	0,0532	0,0418
4206	HELD_FEM_ADR	0,1218	0,1204	0,1193	0,0436	0,0574	0,0434
4206	HELD_ALL_ADR5ULN	0,1204	0,1214	0,1254	0,0472	0,0639	0,0488
4527	CVD_ALL	0,0044	0,0031	0,0012	0,2436	0,2844	0,2451
4527	HELD_FEM_LIP2	0,0441	0,0429	0,0424	0,0147	0,0157	0,0145
4527	HELD_MAL_CC	0,0814	0,0496	0,0661	0,0208	0,0296	0,0197
4527	HELD_MAL_CC2	0,0599	0,0604	0,0583	0,0256	0,0378	0,0267
4527	HELD_ALL_ADR3ULN	0,0688	0,0608	0,0728	0,0316	0,0402	0,0354
4527	HELD_ALL_CC2	0,1329	0,1396	0,1355	0,0449	0,048	0,0461
4527	HELD_ALL_ADR5ULN	0,0796	0,0668	0,1142	0,0478	0,0592	0,0569
4544	HELD_MAL_ADR3ULN	0,0116	0,0154	0,0146	0,0043	0,0062	0,0063
4544	HELD_MAL_ADR	0,0731	0,0643	0,0601	0,0283	0,0348	0,0274
4544	HELD_ALL_ADR	0,086	0,0869	0,0832	0,0279	0,0308	0,0276
4544	HELD_ALL_ADR3ULN	0,1284	0,1257	0,1312	0,0497	0,054	0,0537
4545	HELD_MAL_ADR3ULN	0,0116	0,0154	0,0146	0,0043	0,0062	0,0063
4545	HELD_MAL_ADR	0,0629	0,0569	0,0516	0,0234	0,0247	0,0226
4545	HELD_ALL_ADR	0,0947	0,0982	0,0917	0,0318	0,0385	0,0314
4668	HELD_ALL_ADR5ULN	0,0773	0,0782	0,0348	0,1143	0,1279	0,1111
4669	HELD_FEM_BFF	0,1061	0,1031	0,1053	0,0415	0,0458	0,0412
4718	HELD_MAL_LIP	0,0234	0,0261	0,006	0,2267	0,2838	0,2221
4818	HELD_MAL_LIP	0,0117	0,0073	0,0072	0,0904	0,1138	0,0946
4827	HELD_MAL_ADR5ULN	0,0267	0,0922	0,0873	0,6447	0,708	0,6539
4838	HELD_ALL_CC2	0,1354	0,1425	0,1366	0,047	0,0495	0,0469
4856	CVD_MAL	0,0123	0,0338	0,0089	0,0129	0,0349	0,0094

WAYSNE	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
4868	HELD_MAL_ADR	0,0492	0,055	0,0155	0,2125	0,24	0,2117
4868	HELD_MAL_ADR5ULN	0,0236	0,1201	0,1125	0,412	0,5267	0,4261
4887	HELD_MAL_CC	0,0119	0,0064	0,0075	0,0066	0,0077	0,0042
4887	HELD_ALL_CC	0,0826	0,0705	0,0811	0,0378	0,0429	0,0378
4912	HELD_MAL_LIP	0,2542	0,3163	0,2499	0,0325	0,053	0,0303
4951	HELD_ALL_ADR3ULN	0,0019	0,0018	0,0018	0,5543	0,6301	0,5547
4951	HELD_FEM_ADR3ULN	0,0028	0,0029	0,003	0,237	0,284	0,2372
4951	HELD_FEM_ADR5ULN	0,0049	0,0039	0,0088	0,0663	0,0845	0,0657
4951	HELD_ALL_ADR5ULN	0,006	0,0054	0,0103	0,0586	0,0675	0,0589
4951	HELD_FEM_ADR	0,0104	0,0096	0,0091	0,1202	0,1247	0,12
4951	HELD_ALL_ADR	0,0233	0,0229	0,022	0,1271	0,1376	0,1269
4952	HELD_ALL_ADR3ULN	0,0018	0,0017	0,0015	0,6771	0,7182	0,6774
4952	HELD_FEM_ADR3ULN	0,0019	0,0017	0,002	0,2491	0,2848	0,2496
4952	HELD_FEM_ADR5ULN	0,0029	0,0023	0,0048	0,0938	0,1245	0,094
4952	HELD_ALL_ADR5ULN	0,0062	0,0056	0,009	0,1013	0,1264	0,102
4966	HELD_MAL_LIP	0,0276	0,027	0,0099	0,0138	0,0207	0,0122
4966	HELD_MAL_ADR	0,0409	0,046	0,0375	0,0937	0,1211	0,0933
4966	HELD_FEM_CC	0,0951	0,1056	0,0936	0,0442	0,0696	0,0434
5019	CVD_FEM	0,0011	0,001	0,0007	0,0055	0,0087	0,0053
5019	HELD_ALL_CC2	0,0043	0,0045	0,0043	0,0479	0,0599	0,0477
5019	HELD_MAL_HDL	0,0666	0,0705	0,0594	0,0076	0,0117	0,0068
5019	HELD_ALL_LIP	0,0362	0,0383	0,0342	0,0109	0,0125	0,0108
5019	HELD_MAL_CC2	0,0182	0,0179	0,0186	0,0143	0,0167	0,0138
5165	HELD_FEM_ADR3ULN	0,0193	0,0172	0,0174	0,064	0,0907	0,0714
5165	HELD_MAL_ADR5ULN	0,0267	0,0922	0,0873	0,6447	0,708	0,6539
5165	HELD_FEM_ADR	0,0405	0,0271	0,0268	0,2071	0,2511	0,2059
5165	HELD_FEM_ADR5ULN	0,0414	0,0557	0,0471	0,0836	0,1012	0,101
5278	HELD_MAL_ADR5ULN	0,0556	0,0596	0,1196	0,046	0,0769	0,0577
5287	HELD_FEM_VEFF	0,0487	0,0497	0,0438	0,0093	0,0101	0,0088
5320	CVD_FEM	0,0342	0,0343	0,0283	0,0279	0,0303	0,0274
5324	HELD_FEM_VEFF	0,0912	0,0915	0,0898	0,0318	0,0391	0,0317
5373	HELD_FEM_ADR5ULN	0,0095	0,0124	0,0056	0,0061	0,0088	0,0028

BAYSNP	COMPARISON	CTYPE	CTYPE	CTYPE	ALLELE	ALLELE	ALLELE
		CPVAL	XPVAL	LRVAL	CPVAL	XPVAL	LRVAL
5373	HELD_ALL_ADR5ULN	0,0776	0,0691	0,0342	0,0287	0,0398	0,0217
5375	HELD_FEM_ADR5ULN	0,0092	0,0136	0,0056	0,0058	0,0081	0,0027
5375	HELD_ALL_ADR5ULN	0,138	0,1305	0,0564	0,0585	0,0615	0,0495
5376	HELD_MAL_ADR5ULN	0,0067	0,1212	0,0373	0,0069	0,1212	0,0386
5377	HELD_FEM_ADR	0,0201	0,019	0,019	0,2353	0,2692	0,2345
5377	HELD_FEM_ADR5ULN	0,0497	0,0546	0,0353	0,0289	0,044	0,0203
5517	HELD_MAL_ADR	0,0831	0,1183	0,0317	0,4341	0,6834	0,4294
5518	HELD_FEM_ADR5ULN	0,0341	0,1839	0,0637	0,0346	0,1839	0,0647
5564	CVD_MAL	0,0139	0,0146	0,0159	0,1077	0,1348	0,1057
5569	HELD_MAL_ADR5ULN	0,1012	0,1304	0,0676	0,0445	0,0667	0,0238
5569	HELD_ALL_ADR5ULN	0,1458	0,1504	0,0609	0,0502	0,0672	0,04
5716	HELD_ALL_ADR3ULN	0,0067	0,0064	0,0069	0,0024	0,0025	0,0023
5716	HELD_FEM_ADR3ULN	0,0071	0,0063	0,0059	0,0027	0,0037	0,0024
5716	HELD_ALL_ADR5ULN	0,0248	0,0232	0,0218	0,0092	0,0124	0,0092
5716	HELD_FEM_ADR5ULN	0,0769	0,0784	0,0685	0,0334	0,0412	0,0321
5717	HELD_ALL_ADR5ULN	0,1212	0,1272	0,097	0,0433	0,049	0,0427
5717	CVD_FEM	0,0496	0,0575	0,0431	0,0551	0,0634	0,054
5850	HELD_MAL_CC	0,0304	0,0344	0,0113	0,1197	0,1794	0,1186
5959	CVD_MAL	0,064	0,0647	0,0552	0,0467	0,0678	0,048
6151	HELD_MAL_ADR	0,0502	0,0501	0,0488	0,3223	0,3964	0,3221
6236	HELD_ALL_ADR	0,0472	0,051	0,0424	0,0867	0,0953	0,0864
6277	HELD_FEM_ADR5ULN	0,0014	0,0053	0,0049	0,0127	0,0215	0,0185
6277	HELD_ALL_ADR5ULN	0,0041	0,0135	0,026	0,0832	0,1012	0,0964
6277	HELD_FEM_ADR	0,0251	0,0239	0,0079	0,0157	0,0186	0,0149
6277	HELD_FEM_ADR3ULN	0,0147	0,0126	0,0119	0,0167	0,02	0,0196
6313	HELD_FEM_UEFF	0,0369	0,0357	0,0376	0,1201	0,1519	0,1204
6369	HELD_FEM_LIP	0,1311	0,145	0,1269	0,0461	0,0594	0,0457
6374	HELD_ALL_ADR3ULN	0,0338	0,0325	0,0352	0,0091	0,0107	0,0099
6374	HELD_MAL_ADR3ULN	0,0498	0,0564	0,044	0,011	0,0152	0,0121
6396	HELD_MAL_CC	0,0165	0,0238	0,0048	0,0233	0,031	0,0066
6396	HELD_ALL_CC	0,0528	0,0316	0,0496	0,0334	0,0403	0,0323
6396	CVD_FEM	0,1144	0,0874	0,0928	0,046	0,0631	0,0442

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IBAYSNP	COMPARISON	CTYPE CPVAL	CTYPE XPVAL	CTYPE LCPVAL	ALLELE CEVAL	ALLELE XPVAL	ALLELE LCPVAL
6396	CVD_ALL	0,1388	0,1213	0,0933	0,0516	0,0541	0,0465
6486	HELD_ALL_CC2	0,1446	0,1479	0,1283	0,0373	0,0528	0,0345
6520	HELD_MAL_ADR5ULN	0,0003	0,0081	0,0068	0,1889	0,3068	0,2137
6520	HELD_MAL_ADR3ULN	0,0021	0,005	0,0051	0,1797	0,2122	0,1939
6520	HELD_ALL_ADR5ULN	0,022	0,0339	0,0666	0,0816	0,0892	0,093
6520	HELD_MAL_ADR	0,0743	0,0876	0,0283	0,322	0,3417	0,3212
6522	HELD_FEM_ADR3ULN	0,0618	0,0604	0,0447	0,2761	0,3091	0,284
6522	HELD_FEM_ADR	0,0523	0,0465	0,0502	0,0894	0,0983	0,0882
6524	HELD_MAL_ADR3ULN	0,0215	0,0213	0,0096	0,0128	0,0173	0,0106
6596	HELD_FEM_ADR3ULN	0	0	0	0	0,0001	0
6596	HELD_FEM_ADR5ULN	0,0001	0,0006	0,0004	0,0001	0,0011	0,0008
6596	HELD_ALL_ADR3ULN	0,0003	0,0006	0,0005	0,0005	0,001	0,001
6596	HELD_FEM_ADR	0,0008	0,0011	0,0005	0,0014	0,0018	0,0009
6596	HELD_ALL_ADR5ULN	0,0025	0,0064	0,0064	0,0036	0,0085	0,0094
6596	HELD_ALL_ADR	0,0199	0,0229	0,0186	0,0253	0,0286	0,0236
6734	HELD_ALL_CC	0,04	0,0752	0,0208	0,0463	0,0816	0,0241
6743	HELD_ALL_ADR	0,0299	0,0298	0,0293	0,5743	0,6388	0,5742
7128	HELD_ALL_ADR3ULN	0,0099	0,0103	0,0081	0,0032	0,0042	0,0021
7128	HELD_FEM_ADR3ULN	0,0161	0,014	0,0134	0,011	0,0121	0,0085
7128	HELD_ALL_ADR5ULN	0,0787	0,0793	0,0702	0,029	0,0316	0,0217
7128	HELD_FEM_ADR	0,0447	0,0497	0,0437	0,0497	0,0519	0,0496
7128	HELD_FEM_ADR5ULN	0,0996	0,1085	0,0925	0,0561	0,0763	0,0458
7363	HELD_FEM_LIP	0,0763	0,0816	0,0701	0,0282	0,0385	0,0276
7363	HELD_ALL_LIP	0,0741	0,0762	0,0712	0,0298	0,0314	0,0299
7409	HELD_FEM_ADR5ULN	0,0051	0,0049	0,01	0,0025	0,0051	0,0054
7409	HELD_FEM_ADR3ULN	0,0303	0,0175	0,0316	0,0135	0,0165	0,0172
7409	HELD_MAL_ADR5ULN	0,1823	0,1987	0,0669	0,0691	0,128	0,017
8138	HELD_MAL_LIP	0,0177	0,0193	0,0183	0,0079	0,0088	0,0069
8138	HELD_MAL_CC	0,0107	0,011	0,0077	0,4323	0,4651	0,4318
8138	HELD_ALL_LIP	0,0401	0,039	0,0399	0,0761	0,0923	0,0757
8168	HELD_MAL_LIP	0,0229	0,0222	0,026	0,011	0,0203	0,0132
8168	HELD_FEM_LIP	0,0241	0,0204	0,0226	0,1027	0,1374	0,1017

BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALTELL CPVAL	ALTELL XPVAL	ALTELL LRPVAL
8210	HELD_ALL_ADR3ULN	0,0096	0,0098	0,0098	0,7816	0,8049	0,7818
8210	HELD_FEM_ADR3ULN	0,0141	0,0135	0,0159	0,4056	0,4314	0,4063
8210	HELD_FEM_ADR	0,0222	0,0225	0,0198	0,2153	0,2257	0,2151
8210	HELD_ALL_ADR	0,0215	0,021	0,0203	0,2277	0,2424	0,2276
8241	HELD_FEM_LIP	0,0187	0,0132	0,0085	0,0063	0,0082	0,0058
8241	HELD_ALL_LIP	0,159	0,1538	0,1542	0,0425	0,0474	0,0407
8249	HELD_ALL_ADR3ULN	0,0387	0,0449	0,0478	0,0458	0,0517	0,0569
8249	HELD_ALL_ADR5ULN	0,0455	0,0847	0,0653	0,0527	0,0943	0,0765
8480	CVD_FEM	0,0462	0,0244	0,0232	0,0026	0,0039	0,0008
8480	CVD_MAL	0,1317	0,1542	0,0466	0,0145	0,0286	0,0026
8577	HELD_ALL_ADR3ULN	0,067	0,0657	0,0615	0,0252	0,0333	0,0264
8577	HELD_ALL_ADR	0,0786	0,0752	0,0779	0,0341	0,0374	0,0339
8577	HELD_ALL_ADR5ULN	0,1543	0,1417	0,1606	0,05	0,0577	0,0532
8578	HELD_ALL_ADR3ULN	0,0857	0,0895	0,0777	0,0407	0,0491	0,0421
8653	HELD_MAL_ADR	0,0015	0,002	0,0012	0,004	0,005	0,0032
8653	HELD_MAL_ADR3ULN	0,0104	0,0118	0,0049	0,0239	0,0259	0,0099
8653	HELD_MAL_ADR5ULN	0,0243	0,0358	0,0061	0,0499	0,0688	0,0107
8653	HELD_ALL_ADR3ULN	0,0509	0,0714	0,04	0,0799	0,1109	0,0679
8816	HELD_FEM_LIP2	0,0115	0,0116	0,0106	0,0057	0,0067	0,0056
8816	HELD_FEM_HDL	0,0254	0,0258	0,0184	0,0126	0,0148	0,0119
8816	HELD_ALL_CC2	0,0198	0,0205	0,0188	0,0352	0,0373	0,0354
8816	CVD_ALL	0,0862	0,084	0,0801	0,0253	0,0334	0,0231
8816	HELD_FEM_CC2	0,0732	0,0788	0,0699	0,0263	0,0349	0,0263
8816	HELD_MAL_HDL	0,0827	0,0805	0,0459	0,9552	1	0,9552
8931	HELD_FEM_ADR3ULN	0,0638	0,0558	0,0365	0,1009	0,1129	0,0851
8943	HELD_MAL_ADR3ULN	0,115	0,1264	0,0702	0,0366	0,0409	0,0217
9243	HELD_FEM_VEFF	0,0407	0,0439	0,0252	0,155	0,1691	0,1544
9243	HELD_MAL_ADR5ULN	0,1035	0,0777	0,0285	0,2159	0,2497	0,1855
9243	HELD_FEM_UEFF	0,1004	0,12	0,0335	0,1733	0,2118	0,1696
9523	HELD_MAL_ADR5ULN	0,0425	0,0646	0,0613	0,0575	0,0785	0,0889
9940	HELD_MAL_CC	0,0213	0,0425	0,0073	0,0294	0,0542	0,0099
9940	HELD_ALL_CC	0,0341	0,0266	0,0312	0,0231	0,0354	0,0225

BAYSNT	COMPARISON	GTTYPE CPVAL	GTTYPE XPVAL	GTTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
10091	HELD_ALL_ADR3ULN	0,0852	0,0819	0,1028	0,0428	0,0524	0,0487
10541	HELD_FEM_UEFF	0,0349	0,0191	0,0267	0,0305	0,0477	0,0256
10541	HELD_FEM_VEFF	0,066	0,0484	0,0643	0,0206	0,0217	0,02
10600	CVD_MAL	0,0475	0,0359	0,0348	0,0046	0,0121	0,0029
10600	HELD_ALL_HDL	0,0207	0,0298	0,0058	0,0231	0,0325	0,0064
10600	HELD_MAL_HDL	0,056	0,1137	0,0231	0,0625	0,1228	0,0256
10745	HELD_MAL_LIP	0,0926	0,0862	0,085	0,056	0,0701	0,0491
10748	HELD_MAL_LIP	0,1405	0,1855	0,1371	0,05	0,0676	0,0547
10749	HELD_FEM_LIP	0,0593	0,0591	0,055	0,0232	0,026	0,023
10785	CVD_MAL	0,1111	0,1415	0,1247	0,0383	0,0491	0,0448
10811	HELD_FEM_LIP2	0,0827	0,0859	0,0821	0,0442	0,0465	0,0435
10811	CVD_ALL	0,1149	0,1091	0,1111	0,0524	0,0646	0,0498
10830	HELD_ALL_LIP2	0,0065	0,0065	0,0062	0,0036	0,0039	0,0036
10830	HELD_ALL_LIP	0,0187	0,0191	0,018	0,0037	0,0048	0,0037
10830	HELD_MAL_LIP2	0,0389	0,0395	0,0383	0,011	0,0112	0,0109
10830	CVD_FEM	0,0268	0,0239	0,0238	0,0125	0,0141	0,0121
10830	HELD_MAL_LIP	0,0742	0,0873	0,0613	0,0224	0,0279	0,0219
10830	HELD_FEM_LIP	0,1364	0,1403	0,134	0,0428	0,0556	0,0426
10949	HELD_FEM_VEFF	0,0543	0,0577	0,0536	0,0352	0,0374	0,0351
10949	HELD_FEM_EFF	0,0748	0,0744	0,0743	0,0356	0,04	0,0356
10962	CVD_FEM	0,0113	0,0275	0,0091	0,0218	0,0457	0,0177
10962	HELD_ALL_ADR3ULN	0,1473	0,1615	0,043	0,2642	0,3199	0,258
10966	HELD_ALL_ADR3ULN	0,1289	0,1277	0,0351	0,1511	0,1736	0,1447
10966	HELD_ALL_ADR5ULN	0,1509	0,1612	0,0683	0,0587	0,0794	0,0483
11000	HELD_MAL_LIP2	0,0379	0,0378	0,0375	0,0125	0,0143	0,0123
11000	CVD_FEM	0,0202	0,0198	0,0161	0,9584	1	0,9584
11000	HELD_MAL_ADR3ULN	0,0414	0,0384	0,0554	0,0307	0,0378	0,0344
11000	HELD_ALL_LIP2	0,0965	0,0965	0,096	0,0351	0,0358	0,0348
11000	HELD_MAL_ADR5ULN	0,0477	0,0555	0,0971	0,053	0,0607	0,0618
11001	HELD_MAL_LIP2	0,03	0,0288	0,0297	0,0103	0,0111	0,0102
11001	HELD_ALL_LIP2	0,0662	0,0652	0,0658	0,0235	0,0241	0,0232
11001	CVD_FEM	0,0325	0,0293	0,0266	0,9749	1	0,9749

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EASISNP	COMPARISON	CTYPE	GTYPE	GTYPE	ALLELE	ALLELE	ALLELE
		CPVAL	MPVAL	LRPVAL	CPVAL	MPVAL	LRPVAL
11001	HELD_MAL_ADR3ULN	0,0414	0,0384	0,0554	0,0307	0,0378	0,0344
11001	HELD_ALL_LIP	0,1116	0,1195	0,1013	0,0482	0,057	0,0473
11020	HELD_MAL_ADR3ULN	0,1685	0,1457	0,087	0,0596	0,0761	0,049
11073	HELD_FEM_LIP	0,111	0,1116	0,1085	0,0331	0,0361	0,0328
11073	HELD_ALL_CC2	0,096	0,0963	0,0954	0,0453	0,0475	0,0437
11192	HELD_FEM_ADR5ULN	0,0153	0,0191	0,0329	0,2812	0,2901	0,2893
11192	HELD_FEM_ADR3ULN	0,0257	0,0216	0,0353	0,2446	0,3079	0,249
11248	HELD_FEM_ADR3ULN	0,0183	0,0153	0,0137	0,025	0,0322	0,0203
11248	HELD_ALL_ADR	0,1078	0,1144	0,1071	0,042	0,0434	0,0419
11410	HELD_FEM_VEFF	0,0091	0,0089	0,0085	0,088	0,0909	0,0879
11448	HELD_MAL_HDL	0,0019	0,0012	0,0015	0,0002	0,0003	0,0002
11448	HELD_MAL_LIP	0,0055	0,0027	0,0061	0,0034	0,005	0,0042
11448	HELD_MAL_LIP2	0,0059	0,0056	0,0058	0,0233	0,0245	0,0234
11448	HELD_ALL_LIP2	0,0108	0,0106	0,0109	0,0119	0,0124	0,012
11448	HELD_ALL_HDL	0,0647	0,0708	0,0648	0,0138	0,0215	0,0142
11448	HELD_FEM_ADR	0,0637	0,0601	0,0603	0,0162	0,0199	0,0156
11448	HELD_ALL_ADR	0,0576	0,0568	0,055	0,017	0,0209	0,0166
11448	HELD_ALL_CC	0,0976	0,1314	0,0453	0,0671	0,0727	0,0652
11450	HELD_MAL_LIP	0,0068	0,0052	0,0066	0,0007	0,0012	0,0009
11456	CVD_FEM	0,0026	0,0043	0,0016	0,0038	0,0058	0,0023
11462	HELD_MAL_LIP2	0,0302	0,0225	0,0284	0,0091	0,0109	0,0091
11462	HELD_ALL_LIP2	0,0406	0,0368	0,0362	0,0384	0,0431	0,0387
11483	HELD_FEM_ADR5ULN	0,032	0,0455	0,0589	0,0562	0,0771	0,0832
11483	HELD_FEM_ADR3ULN	0,0442	0,034	0,0495	0,0824	0,0989	0,0958
11483	HELD_FEM_ADR	0,0628	0,0468	0,045	0,1531	0,2	0,1477
11531	HELD_FEM_CC	0,1229	0,1273	0,0498	0,0189	0,0335	0,0137
11536	HELD_ALL_CC	0,0789	0,085	0,0365	0,7564	0,8525	0,7562
11537	HELD_MAL_ADR	0,1696	0,1625	0,1616	0,0467	0,0604	0,0455
11558	HELD_MAL_LIP2	0,0028	0,0023	0,0028	0,0058	0,0064	0,0058
11558	HELD_ALL_LIP2	0,011	0,0105	0,011	0,005	0,0054	0,005
11558	HELD_ALL_CC	0,0533	0,0503	0,05	0,102	0,1242	0,1013
11585	HELD_MAL_CC	0,0414	0,0372	0,0136	0,0108	0,0193	0,0094

BAYSNP	COMPARISON	GTTYPE CPVAL	GTTYPE XPVAL	GTTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
11594	HELD_ALL_ADR3ULN	0,0819	0,0998	0,035	0,0195	0,0196	0,0069
11594	HELD_MAL_ADR	0,0312	0,0403	0,0277	0,0365	0,0462	0,0324
11614	HELD_FEM_CC	0,0473	0,0577	0,0234	0,0572	0,0644	0,0587
11614	HELD_MAL_CC2	0,052	0,0518	0,0331	0,0346	0,0482	0,0373
11614	HELD_ALL_CC	0,0923	0,1151	0,0429	0,25	0,2653	0,2502
11614	HELD_ALL_HDL	0,0563	0,0558	0,0499	0,9149	1	0,9149
11631	HELD_MAL_ADR5ULN	0,0386	0,0478	0,0304	0,0117	0,0156	0,0155
11631	HELD_MAL_ADR3ULN	0,1371	0,1283	0,1422	0,046	0,0572	0,051
11637	HELD_FEM_LIP	0,0168	0,0155	0,0113	0,0321	0,0343	0,0317
11637	HELD_ALL_LIP	0,0303	0,0314	0,0288	0,0148	0,0186	0,0149
11637	CVD_MAL	0,0697	0,0701	0,0767	0,0248	0,0373	0,0272
11637	CVD_ALL	0,0723	0,0759	0,073	0,0254	0,0318	0,0262
11641	HELD_MAL_ADR	0,0142	0,0141	0,0129	0,126	0,1468	0,1257
11645	HELD_FEM_CC	0,0369	0,0544	0,0366	0,0456	0,0639	0,0454
11646	HELD_FEM_LIP	0,0865	0,0938	0,0854	0,0359	0,0387	0,0356
11646	HELD_ALL_LIP	0,0788	0,077	0,078	0,0438	0,0453	0,0431
11652	HELD_MAL_LIP	0,0422	0,0402	0,0403	0,9398	1	0,9398
11727	HELD_ALL_ADR5ULN	0,0133	0,0169	0,001	0,0033	0,0029	0,0001
11727	HELD_MAL_ADR3ULN	0,0139	0,0156	0,0019	0,0035	0,0042	0,0002
11727	HELD_MAL_ADR5ULN	0,0632	0,0556	0,0165	0,0205	0,0202	0,003
11727	HELD_ALL_ADR3ULN	0,0384	0,0373	0,0163	0,0076	0,0071	0,0036
11727	HELD_FEM_ADR5ULN	0,1918	0,2611	0,0649	0,0728	0,128	0,0182
11728	HELD_ALL_ADR5ULN	0,1462	0,1458	0,095	0,0556	0,0654	0,0388
11914	HELD_MAL_ADR3ULN	0,2466	0,3289	0,2216	0,0257	0,0387	0,0248
11938	HELD_ALL_ADR3ULN	0,0089	0,0095	0,0046	0,392	0,459	0,3897
11938	HELD_ALL_ADR5ULN	0,0169	0,0157	0,0114	0,8154	0,8766	0,815
11938	HELD_FEM_ADR3ULN	0,0449	0,0479	0,0352	0,6253	0,6469	0,6247
11950	HELD_MAL_ADR5ULN	0,0201	0,0516	0,0044	0,0125	0,0113	0,0014
11950	HELD_MAL_ADR3ULN	0,0154	0,0166	0,0066	0,0323	0,0548	0,0214
11950	HELD_MAL_ADR	0,0516	0,0613	0,0496	0,3586	0,4444	0,3582
11951	HELD_MAL_ADR5ULN	0,0424	0,0545	0,0114	0,0236	0,0423	0,0037
11951	HELD_FEM_UEFF	0,0259	0,0235	0,0107	0,0733	0,0868	0,0749

DATA SNR	COMPARISON	GTVAL	SHVAL	GEVAL	AL1VAL	AL2VAL	AL3VAL
		CPVAL	XPVAL	ERPVAL	GEVAL	XPVAL	ERPVAL
12008	HELD_ALL_ADR	0,0485	0,062	0,0449	0,0524	0,0663	0,0486
12031	HELD_ALL_ADR3ULN	0,0028	0,0024	0,0026	0,63	0,7148	0,6303
12031	HELD_FEM_ADR5ULN	0,0046	0,0039	0,0086	0,0566	0,0838	0,0562
12031	HELD_ALL_ADR5ULN	0,0047	0,0041	0,0086	0,0504	0,0658	0,0508
12031	HELD_FEM_ADR3ULN	0,0056	0,0063	0,006	0,2925	0,3532	0,2929
12031	HELD_ALL_ADR	0,0138	0,0141	0,0129	0,1033	0,113	0,1031
12031	HELD_FEM_ADR	0,0147	0,0143	0,0131	0,1206	0,1247	0,1203
12032	HELD_FEM_UEFF	0,0304	0,0139	0,0261	0,0076	0,0093	0,0078
12032	HELD_FEM_ADR	0,1261	0,1063	0,0841	0,0343	0,0448	0,031
12032	HELD_ALL_ADR	0,0928	0,0748	0,0517	0,0359	0,0376	0,0341
12032	HELD_FEM_VEFF	0,0639	0,0469	0,0614	0,0748	0,0929	0,0737
12148	HELD_MAL_ADR5ULN	0,0166	0,0158	0,026	0,0087	0,0155	0,0126
12148	HELD_MAL_ADR	0,0376	0,0431	0,0328	0,0142	0,0207	0,0139
12148	HELD_MAL_ADR3ULN	0,0616	0,0647	0,085	0,0349	0,046	0,0398
12207	HELD_MAL_ADR5ULN	0,0034	0,0036	0,002	0,6147	0,7792	0,6195
12207	HELD_MAL_ADR	0,003	0,0028	0,002	0,1131	0,1259	0,1125
12207	HELD_MAL_ADR3ULN	0,024	0,0181	0,0298	0,5888	0,6671	0,5919
12399	HELD_MAL_ADR5ULN	0,0204	0,0336	0,0287	0,0338	0,0497	0,0552
12399	HELD_MAL_ADR3ULN	0,0366	0,0602	0,0433	0,0568	0,0858	0,0714
12399	HELD_ALL_ADR	0,1174	0,109	0,1156	0,0393	0,0481	0,0386
12554	HELD_MAL_ADR	0,0489	0,0266	0,0384	0,0217	0,0303	0,0198
12554	HELD_FEM_VEFF	0,0785	0,0754	0,0774	0,0335	0,0365	0,0329
12851	HELD_FEM_ADR5ULN	0,0841	0,0704	0,087	0,0401	0,0635	0,0488
12851	HELD_MAL_ADR	0,0496	0,0509	0,0432	0,6573	0,6625	0,6573
13025	HELD_MAL_ADR3ULN	0,0572	0,0578	0,0424	0,8568	1	0,8564
13025	HELD_FEM_ADR5ULN	0,0508	0,0491	0,0749	0,2494	0,3182	0,2546
13191	HELD_ALL_CC	0,0795	0,0789	0,0666	0,0287	0,0329	0,0278
13192	HELD_MAL_ADR3ULN	0,0028	0,0047	0,0052	0,2629	0,3274	0,2753
13192	HELD_MAL_ADR5ULN	0,0306	0,0985	0,1047	0,6516	0,7437	0,6584
13192	HELD_ALL_ADR3ULN	0,0459	0,0411	0,0633	0,9559	1	0,9559
13192	HELD_MAL_ADR	0,0927	0,0909	0,0428	0,7098	0,743	0,7097
13193	HELD_MAL_ADR3ULN	0,0022	0,0038	0,0046	0,2596	0,3258	0,2719

PAVSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	ALF00LE CEVAL	ALF00LE XPVAL	ALF00LE LRPVAL
13193	HELD_MAL_ADR5ULN	0,0227	0,0881	0,1013	0,5694	0,7373	0,5794
13193	HELD_ALL_ADR3ULN	0,0375	0,0347	0,0515	0,9356	1	0,9355
13338	HELD_FEM_UEFF	0,0314	0,033	0,0259	0,5721	0,5935	0,5716
13338	HELD_FEM_VEFF	0,0306	0,0309	0,03	0,8319	0,8624	0,8319
13339	HELD_MAL_ADR	0,0352	0,036	0,011	0,4768	0,5694	0,4767
13339	CVD_FEM	0,1362	0,0953	0,1082	0,0512	0,0803	0,0465
13340	HELD_FEM_VEFF	0,0158	0,0143	0,0137	0,0082	0,0095	0,0072
13479	HELD_FEM_UEFF	0,1063	0,0953	0,1076	0,0341	0,0364	0,0351
13633	HELD_FEM_ADR3ULN	0,0913	0,0763	0,1042	0,0317	0,037	0,0361
13633	HELD_FEM_ADR	0,1138	0,1293	0,1084	0,0387	0,0448	0,0384
13929	HELD_MAL_ADR5ULN	0,2957	0,2981	0,1308	0,1262	0,2119	0,0423
14065	HELD_FEM_EFF	0,087	0,0675	0,0858	0,0307	0,037	0,0303
14083	HELD_FEM_ADR	0,069	0,0657	0,0318	0,0353	0,0459	0,034
14085	HELD_FEM_EFF	0,0345	0,0318	0,0334	0,1267	0,1326	0,126
14087	HELD_FEM_EFF	0,0509	0,0493	0,0504	0,1138	0,1184	0,1138
14102	HELD_MAL_ADR5ULN	0,0062	0,0084	0,0014	0,8445	1	0,844
14102	HELD_FEM_EFF	0,1217	0,124	0,1207	0,0351	0,0391	0,035
14103	HELD_FEM_EFF	0,003	0,0023	0,0004	0,0567	0,0623	0,0565
14103	HELD_FEM_VEFF	0,0371	0,0337	0,0117	0,495	0,5329	0,4948
14103	HELD_FEM_UEFF	0,0605	0,0655	0,0291	0,0747	0,0807	0,076
14129	HELD_ALL_ADR3ULN	0,0384	0,0376	0,0479	0,1413	0,1647	0,1434
14129	HELD_MAL_ADR3ULN	0,0448	0,04	0,0567	0,3415	0,4056	0,3453
14326	HELD_FEM_EFF	0,1463	0,1445	0,1434	0,0461	0,0471	0,0457
14503	HELD_ALL_ADR5ULN	0,0052	0,0046	0,0021	0,6567	0,7349	0,6547
14503	HELD_ALL_ADR3ULN	0,0046	0,0045	0,004	0,5974	0,6922	0,5986
14503	HELD_FEM_ADR5ULN	0,0136	0,0123	0,0063	0,9862	1	0,9862
14503	HELD_FEM_ADR3ULN	0,0203	0,0189	0,0179	0,482	0,5051	0,4834
14537	HELD_ALL_ADR	0,0148	0,0153	0,0133	0,0049	0,0053	0,0048
14537	HELD_FEM_ADR	0,0395	0,0398	0,0332	0,0288	0,0309	0,0284
15915	HELD_FEM_ADR	0,0018	0,0013	0,0012	0,6403	0,6575	0,6405
15915	HELD_ALL_ADR	0,0037	0,0031	0,0029	0,4718	0,5008	0,4719
15915	HELD_ALL_ADR3ULN	0,1292	0,1365	0,0778	0,0267	0,0357	0,021

DAYSNP	COMPARISON	CTYPE CPVAL	CTYPE XPVAL	CTYPE LRPVAL	ASLTYPE CPVAL	ASLTYPE XPVAL	ASLTYPE LRPVAL
19289	HELD_MAL_CC	0,0256	0,0181	0,0109	0,1599	0,2059	0,1642
19289	HELD_ALL_CC	0,0392	0,0216	0,0288	0,0989	0,1133	0,095
19289	HELD_MAL_LIP	0,0974	0,0892	0,0855	0,0474	0,0689	0,0515
36958	HELD_MAL_ADR3ULN	0,0804	0,108	0,0242	0,0926	0,1218	0,0274
37158	HELD_ALL_ADR	0,0266	0,0259	0,0248	0,0076	0,0078	0,0074
37158	HELD_FEM_ADR	0,0547	0,0511	0,047	0,0328	0,0384	0,0323
37160	HELD_FEM_UEFF	0,0494	0,0385	0,0291	0,0206	0,0238	0,0215
37412	HELD_FEM_ADR5ULN	0,0274	0,0301	0,0228	0,0901	0,1029	0,0965
37412	HELD_ALL_ADR5ULN	0,0463	0,0416	0,0443	0,1444	0,1838	0,1518
37412	HELD_FEM_ADR3ULN	0,1388	0,1374	0,1428	0,0436	0,0523	0,0457
37457	CVD_ALL	0,006	0,0043	0,0045	0,0004	0,0006	0,0005
37457	CVD_FEM	0,0618	0,0475	0,0371	0,0084	0,0138	0,0049
37457	CVD_MAL	0,1106	0,1397	0,1478	0,0425	0,0646	0,0633
37704	HELD_MAL_ADR5ULN	0,0093	0,1304	0,041	0,0096	0,1304	0,0423
38959	CVD_ALL	0,0357	0,0284	0,0234	0,7204	0,8145	0,7186
38959	HELD_FEM_EFF	0,0937	0,0903	0,0433	0,1155	0,1245	0,1149
39292	HELD_FEM_ADR5ULN	0,0461	0,0797	0,1143	0,0295	0,0406	0,0445
39292	HELD_ALL_ADR5ULN	0,2107	0,197	0,2673	0,0487	0,0566	0,0656
39698	HELD_MAL_ADR3ULN	0,0549	0,0575	0,0339	0,1964	0,2316	0,1955
39756	HELD_FEM_ADR3ULN	0,1838	0,1894	0,1779	0,0494	0,069	0,0449
39951	HELD_MAL_ADR	0,0126	0,0133	0,0027	0,1824	0,227	0,1816
39951	HELD_ALL_ADR	0,0036	0,0033	0,0031	0,7179	0,7614	0,7178
39951	HELD_FEM_ADR	0,0243	0,023	0,0233	0,0941	0,102	0,0932
39951	HELD_FEM_ADR5ULN	0,0673	0,0646	0,0583	0,0366	0,0423	0,0421
40466	HELD_FEM_EFF	0,0024	0,002	0,0009	0,0045	0,0058	0,0044
40466	HELD_FEM_UEFF	0,0802	0,0728	0,0265	0,0419	0,0518	0,0382
40466	HELD_FEM_VEFF	0,0511	0,0458	0,0386	0,0313	0,0339	0,0309
44442	HELD_MAL_ADR5ULN	0,0836	0,079	0,0743	0,0364	0,0585	0,0418
55504	HELD_MAL_ADR	0,0719	0,0735	0,0691	0,0286	0,0345	0,0284
55542	HELD_FEM_ADR	0,0351	0,0377	0,0327	0,0223	0,0271	0,0221
55670	HELD_FEM_VEFF	0,0177	0,0252	0,0172	0,0215	0,03	0,0208
55736	HELD_ALL_ADR5ULN	0,0576	0,0583	0,0098	0,0205	0,0356	0,0023

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BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE TERPVAL	ALTEFF OPVAL	ALTEFF XRVAL	ALTEFF TERPVAL
55736	HELD_MAL_ADR5ULN	0,0618	0,087	0,0194	0,0901	0,1202	0,0263
55736	HELD_FEM_ADR5ULN	0,3245	0,4065	0,1534	0,1163	0,2053	0,0385
55748	HELD_MAL_ADR5ULN	0,3118	0,3008	0,1412	0,134	0,2136	0,0461
55813	HELD_ALL_ADR3ULN	0,0935	0,0976	0,0867	0,0234	0,0248	0,0235
55845	HELD_FEM_VEFF	0,026	0,0242	0,0254	0,0129	0,0138	0,0128
55845	HELD_MAL_ADR3ULN	0,0952	0,0988	0,0453	0,0432	0,0619	0,0372
55845	HELD_FEM_UEFF	0,1378	0,142	0,1358	0,045	0,0588	0,0453
55923	HELD_FEM_ADR	0,0587	0,058	0,0556	0,0191	0,0224	0,0187
55923	HELD_FEM_ADR3ULN	0,0606	0,0562	0,0659	0,0213	0,0267	0,0222
55945	HELD_FEM_ADR	0,0125	0,0109	0,0112	0,0031	0,0035	0,003
55945	HELD_FEM_ADR3ULN	0,0381	0,0379	0,0442	0,0127	0,0185	0,0137
55945	HELD_ALL_ADR	0,0809	0,0801	0,0782	0,0292	0,0327	0,029
56007	HELD_MAL_ADR3ULN	0,0308	0,0293	0,005	0,1915	0,2107	0,1828
56007	HELD_MAL_ADR5ULN	0,139	0,1477	0,0466	0,2654	0,2957	0,2514
56011	HELD_ALL_ADR5ULN	0,1056	0,2178	0,0322	0,1135	0,2277	0,0343
56104	HELD_FEM_UEFF	0,0155	0,0153	0,0149	0,0164	0,0198	0,0166
56113	HELD_ALL_ADR5ULN	0,0186	0,0163	0,0264	0,0347	0,0387	0,0352
56113	HELD_ALL_ADR3ULN	0,0285	0,029	0,0276	0,3219	0,3794	0,3228
56113	HELD_FEM_ADR5ULN	0,0402	0,0472	0,0536	0,036	0,0498	0,0358
56113	HELD_FEM_ADR3ULN	0,0416	0,0401	0,0432	0,1311	0,1519	0,1314
56636	HELD_FEM_ADR	0,0108	0,0106	0,0098	0,5577	0,6169	0,5576
56636	HELD_FEM_ADR3ULN	0,0227	0,0223	0,0215	0,7019	0,7532	0,7016
56636	HELD_FEM_ADR5ULN	0,0271	0,0247	0,027	0,8077	0,8498	0,8079
56666	HELD_MAL_ADR3ULN	0,2121	0,3446	0,0763	0,0154	0,0133	0,0018
56666	HELD_MAL_ADR5ULN	0,3794	0,418	0,1913	0,0556	0,0716	0,0122
56666	HELD_MAL_ADR	0,1717	0,119	0,136	0,0173	0,0265	0,0154
56667	HELD_FEM_EFF	0,0364	0,0372	0,0356	0,0134	0,014	0,0133
56667	HELD_MAL_ADR3ULN	0,2981	0,4124	0,2471	0,0382	0,0579	0,0311
56667	HELD_FEM_ADR3ULN	0,1228	0,1267	0,1124	0,0483	0,0586	0,0492
56780	HELD_FEM_ADR3ULN	0,0149	0,0159	0,008	0,012	0,0164	0,0117
56780	HELD_FEM_ADR	0,0227	0,0214	0,0192	0,012	0,0154	0,0118
56780	HELD_ALL_ADR3ULN	0,0269	0,0274	0,019	0,0143	0,0182	0,0141

FEAT/STP	COMPARISON	CTYPE CPVAL	CTYPE XPVAL	CTYPE LRPVAL	ALIEFF CPVAL	ALIEFF XPVAL	ALIEFF LRPVAL
56780	HELD_ALL_ADR	0,0842	0,0843	0,0808	0,0435	0,0453	0,0433
56876	HELD_FEM_UEFF	0,0372	0,0266	0,0308	0,0169	0,0232	0,0141
56876	HELD_FEM_EFF	0,0424	0,0386	0,0418	0,0166	0,0177	0,0163
56876	HELD_FEM_VEFF	0,0713	0,0569	0,0692	0,0196	0,0216	0,0192
56978	HELD_ALL_ADR5ULN	0,0719	0,0767	0,0535	0,0154	0,0156	0,0118
57000	HELD_FEM_VEFF	0,0174	0,0176	0,0169	0,3734	0,4158	0,3731
57000	HELD_FEM_UEFF	0,0415	0,0406	0,0369	0,858	0,8914	0,8579
57000	CVD_ALL	0,0418	0,0488	0,0445	0,0607	0,0713	0,0637
57000	CVD_MAL	0,0441	0,0754	0,0552	0,1657	0,2666	0,1782
57313	HELD_FEM_UEFF	0,034	0,0307	0,0344	0,1193	0,15	0,1201
57734	HELD_FEM_ADR3ULN	0,1496	0,1859	0,1593	0,0475	0,0622	0,0534
57837	HELD_MAL_ADR3ULN	0,1875	0,2505	0,1226	0,0606	0,0663	0,0405
57853	HELD_FEM_EFF	0,0026	0,0022	0,0012	0,0086	0,0107	0,0084
57853	HELD_FEM_UEFF	0,0504	0,0448	0,0138	0,0301	0,0444	0,0274
57853	HELD_FEM_VEFF	0,042	0,0386	0,0288	0,0505	0,0562	0,0501
57854	HELD_FEM_EFF	0,0212	0,0209	0,0157	0,0665	0,0761	0,0663
57854	HELD_FEM_UEFF	0,0736	0,0661	0,0242	0,0496	0,068	0,0464
57854	HELD_MAL_ADR3ULN	0,1957	0,2011	0,1232	0,0634	0,0859	0,0467
58295	HELD_MAL_ADR	0,0215	0,0221	0,0192	0,0596	0,0793	0,0593
58402	HELD_MAL_ADR3ULN	0,253	0,3601	0,2207	0,0277	0,0317	0,0255
58407	HELD_FEM_VEFF	0,009	0,0089	0,0086	0,6756	0,7344	0,6756
58407	HELD_FEM_UEFF	0,0269	0,0254	0,019	0,1833	0,1983	0,1819
58440	HELD_FEM_UEFF	0,1021	0,1012	0,1022	0,0294	0,0358	0,0305
58525	HELD_FEM_ADR	0,0008	0,0004	0,0004	0,0002	0,0003	0,0001
58525	HELD_FEM_ADR3ULN	0,0005	0,0002	0,0008	0,0002	0,0006	0,0005
58525	HELD_FEM_ADR5ULN	0,0002	0,0005	0,0011	0,0009	0,0042	0,0034
58525	HELD_ALL_ADR	0,0309	0,0274	0,0284	0,0041	0,005	0,0037
58525	HELD_ALL_ADR5ULN	0,0115	0,0352	0,0209	0,0263	0,0423	0,0412
58525	HELD_ALL_ADR3ULN	0,0304	0,0391	0,0408	0,0158	0,0198	0,021
58533	HELD_FEM_ADR	0,0132	0,0076	0,011	0,0024	0,0033	0,0019
58533	HELD_FEM_ADR3ULN	0,0373	0,0325	0,0534	0,0101	0,0153	0,0155
58533	HELD_FEM_ADR5ULN	0,0255	0,0368	0,0556	0,0387	0,0613	0,0658

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BAVSNP	COMPARISON	CTYPE CPVAL	CTYPE XPVAL	CTYPE LRPVAL	ALLELE CPVAL	ALLELE XPVAL	ALLELE LRPVAL
58533	HELD_ALL_ADR	0,1948	0,2046	0,1921	0,0446	0,0584	0,0438
58544	HELD_MAL_ADR5ULN	0,2134	0,1955	0,0875	0,0754	0,1197	0,02
58716	HELD_MAL_ADR3ULN	0,0222	0,0288	0,011	0,0012	0,0018	0,0003
58716	HELD_MAL_ADR5ULN	0,1918	0,256	0,1602	0,0649	0,0886	0,047
58736	HELD_FEM_EFF	0,0378	0,0385	0,0374	0,0117	0,0131	0,0117
58808	HELD_FEM_ADR	0,0754	0,076	0,0739	0,0276	0,0333	0,0275
58809	HELD_MAL_ADR5ULN	0,1338	0,1368	0,0404	0,0454	0,0777	0,0088
58809	HELD_ALL_ADR3ULN	0,0117	0,011	0,0202	0,0915	0,1137	0,099
58809	HELD_MAL_ADR3ULN	0,0206	0,0207	0,0247	0,2401	0,3238	0,253
58809	HELD_FEM_UEFF	0,1023	0,1072	0,0586	0,0482	0,0528	0,0446
58886	HELD_FEM_ADR3ULN	0,0432	0,0444	0,0387	0,0115	0,0145	0,0107
58886	HELD_ALL_ADR3ULN	0,0611	0,0627	0,0549	0,0171	0,0233	0,0168
58886	HELD_ALL_ADR5ULN	0,1212	0,1272	0,097	0,0433	0,049	0,0427
58926	HELD_MAL_ADR3ULN	0,0186	0,0222	0,0152	0,0031	0,005	0,0036
58926	HELD_ALL_ADR5ULN	0,0504	0,0525	0,0476	0,0108	0,0121	0,0117
58926	CVD_FEM	0,0461	0,0455	0,0419	0,7899	0,8184	0,7899
58926	HELD_MAL_ADR5ULN	0,1263	0,1409	0,1002	0,0427	0,0517	0,0487
58968	HELD_ALL_ADR5ULN	0,0212	0,0248	0,0199	0,0023	0,003	0,003
58968	HELD_MAL_ADR3ULN	0,0412	0,0375	0,0377	0,0067	0,0098	0,0085
58968	HELD_ALL_ADR3ULN	0,1321	0,1309	0,1338	0,0208	0,028	0,0226
58968	HELD_FEM_ADR5ULN	0,1447	0,1579	0,1408	0,0233	0,0292	0,0261
58985	HELD_ALL_ADR5ULN	0,0341	0,0303	0,0449	0,0085	0,0129	0,0104
59113	HELD_MAL_ADR5ULN	0,0156	0,0224	0,0114	0,0006	0,0008	0,0003
59113	HELD_MAL_ADR3ULN	0,0577	0,0875	0,0558	0,0073	0,009	0,0068
59236	HELD_ALL_ADR	0,0163	0,0158	0,0148	0,0638	0,077	0,0636
59236	HELD_ALL_ADR3ULN	0,0152	0,0151	0,017	0,3664	0,3858	0,3685
59236	HELD_FEM_ADR	0,0242	0,0266	0,0221	0,0693	0,0722	0,0689
59237	HELD_FEM_VEFF	0,021	0,0197	0,0205	0,9766	1	0,9766
59237	HELD_FEM_EFF	0,0278	0,0283	0,0273	0,5742	0,6002	0,5742
59267	HELD_FEM_UEFF	0,0007	0,0006	0,0005	0,0035	0,0042	0,0036
59352	HELD_MAL_ADR	0,0234	0,0233	0,0219	0,6204	0,6787	0,6203
59352	HELD_ALL_ADR	0,0427	0,0412	0,0406	0,8742	0,925	0,8742

BAYSNP	COMPARISON	GRYPE CPVAL	GRYPE XPVAL	GRYPE LRPVAL	ALCPEF CPVAL	ALCPEF XPVAL	ALCPEF LRPVAL
59363	CVD_MAL	0,0678	0,0736	0,0797	0,0336	0,0422	0,0351
59368	HELD_FEM_ADR	0,0119	0,0127	0,0096	0,0049	0,0053	0,0048
59371	HELD_FEM_VEFF	0,0024	0,0022	0,0021	0,1509	0,1694	0,1508
59371	HELD_FEM_UEFF	0,0098	0,0099	0,0092	0,2681	0,286	0,2686
59372	HELD_MAL_ADR	0,1687	0,1722	0,1609	0,0282	0,042	0,0273
59372	HELD_MAL_ADR3ULN	0,22	0,2638	0,2592	0,0467	0,0804	0,0599
59443	HELD_ALL_ADR5ULN	0,0027	0,0031	0,0018	0,366	0,4699	0,3621
59443	HELD_MAL_ADR5ULN	0,0416	0,036	0,0368	0,877	1	0,877
900080	HELD_FEM_ADR3ULN	0,0248	0,0243	0,0334	0,0078	0,0122	0,011
900080	HELD_FEM_ADR5ULN	0,0307	0,0334	0,0528	0,0422	0,0571	0,0639
900102	HELD_FEM_UEFF	0,0079	0,0078	0,008	0,0043	0,0057	0,0041
900102	HELD_FEM_VEFF	0,0423	0,0413	0,0416	0,0163	0,0185	0,0162
900111	HELD_FEM_UEFF	0,022	0,0232	0,0222	0,0107	0,012	0,0103
900111	HELD_FEM_VEFF	0,0524	0,0496	0,0516	0,0293	0,0351	0,0292
900117	HELD_MAL_LIP	0,049	0,0534	0,022	0,0073	0,0136	0,0043
900118	HELD_FEM_EFF	0,0013	0,0008	0,001	0,0001	0,0002	0,0001
900118	HELD_FEM_VEFF	0,1013	0,0874	0,0978	0,0214	0,0303	0,0206
900118	HELD_FEM_ADR5ULN	0,0424	0,0506	0,0251	0,8579	1	0,8561
900118	HELD_ALL_ADR5ULN	0,0702	0,0623	0,0401	0,653	0,7517	0,6608
900120	HELD_FEM_EFF	0,0101	0,0092	0,007	0,0095	0,0109	0,0093
900121	HELD_FEM_EFF	0,0944	0,0944	0,0922	0,0477	0,0488	0,0476
900123	HELD_ALL_ADR	0,0402	0,0568	0,0164	0,041	0,0576	0,0168
900123	HELD_FEM_ADR	0,0678	0,1074	0,0341	0,0695	0,1089	0,0349
900124	HELD_FEM_EFF	0,0185	0,0181	0,0177	0,0602	0,0663	0,0601
900132	HELD_FEM_ADR	0,0215	0,0178	0,0068	0,2283	0,2679	0,2288
900144	CVD_FEM	0,0319	0,0744	0,0093	0,0361	0,0813	0,0104
900144	HELD_ALL_ADR5ULN	0,1356	0,2119	0,0476	0,1425	0,2202	0,0497
900145	CVD_FEM	0,0702	0,0367	0,0231	0,4142	0,4698	0,4044
900145	HELD_ALL_ADR5ULN	0,1364	0,2117	0,0481	0,1436	0,2203	0,0504
900146	HELD_FEM_ADR5ULN	0,0096	0,017	0,0195	0,0366	0,0413	0,0447
900146	HELD_FEM_CC	0,0751	0,0844	0,0429	0,4385	0,4606	0,4405
900146	HELD_MAL_ADR	0,1074	0,1347	0,0497	0,2672	0,3098	0,2671

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BAYSNP	COMPARISON	GTYPE CPVAL	GTYPE XPVAL	GTYPE LRPVAL	AELELE CPVAL	AELELE XPVAL	AELELE LRPVAL
900147	HELD_ALL_ADR3ULN	0,0572	0,0567	0,0416	0,0133	0,015	0,0104
900147	HELD_FEM_ADR3ULN	0,0435	0,0527	0,0381	0,0166	0,0182	0,0127
900196	HELD_MAL_LIP	0,04	0,0376	0,0365	0,0037	0,0057	0,0039
900196	HELD_FEM_LIP	0,0183	0,019	0,0214	0,0168	0,0301	0,0136
900196	HELD_FEM_ADR3ULN	0,0672	0,0693	0,022	0,0238	0,0276	0,0198
900196	CVD_FEM	0,0398	0,0432	0,0293	1	1	1
900196	CVD_ALL	0,0617	0,0655	0,0425	0,1649	0,2139	0,1618
900200	CVD_FEM	0,0865	0,0948	0,0822	0,0359	0,0545	0,0381
900204	HELD_FEM_EFF	0,0051	0,0054	0,005	0,0195	0,0204	0,0194
900205	HELD_FEM_EFF	0,0128	0,0126	0,0126	0,0746	0,0753	0,0745
900205	CVD_MAL	0,0881	0,0873	0,0279	0,0497	0,0672	0,045
900223	HELD_FEM_ADR	0,1823	0,2018	0,1522	0,0357	0,0826	0,0327
900225	HELD_ALL_ADR5ULN	0,0532	0,0765	0,011	0,0615	0,0864	0,0125
900225	HELD_MAL_ADR3ULN	0,0804	0,108	0,0242	0,0926	0,1218	0,0274
900227	HELD_FEM_ADR5ULN	0,076	0,0933	0,0368	0,0271	0,031	0,0108
900233	HELD_FEM_ADR5ULN	0,0314	0,0303	0,024	0,3185	0,3387	0,3136
900236	HELD_FEM_ADR3ULN	0,0378	0,0275	0,0387	0,0494	0,064	0,0568
900236	HELD_MAL_ADR5ULN	0,2375	0,2927	0,0919	0,0994	0,13	0,0289
900241	HELD_FEM_EFF	0,0225	0,0223	0,0219	0,6377	0,6538	0,6376
900242	HELD_ALL_ADR5ULN	0,0164	0,0165	0,0012	0,0015	0,0017	0
900242	HELD_ALL_ADR3ULN	0,0158	0,0151	0,0031	0,0007	0,0006	0,0002
900242	HELD_FEM_ADR5ULN	0,0257	0,0467	0,0032	0,0088	0,0105	0,0007
900242	HELD_MAL_ADR3ULN	0,1963	0,3073	0,0673	0,0132	0,0144	0,0014
900242	HELD_FEM_ADR	0,0219	0,0117	0,0142	0,006	0,0067	0,0053
900242	HELD_FEM_ADR3ULN	0,0542	0,0556	0,0305	0,0161	0,0247	0,0091
900242	HELD_ALL_ADR	0,0373	0,0359	0,0352	0,0146	0,0152	0,0142
900242	HELD_MAL_ADR5ULN	0,416	0,4311	0,2189	0,0691	0,1332	0,0165

Table 6a Correlation of genotypes of PA SNPs to relative risk

For diagnostic conclusions to be drawn from genotyping a particular patient we calculated the relative risk RR1, RR2, RR3 for the three possible genotypes of each SNP. Given the genotype frequencies as

	gtype1	gtype2	gtype3
case	N11	N12	N13
control	N21	N22	N23

we calculate

$$RR1 = \frac{N11}{N21} \bigg/ \frac{N12 + N13}{N22 + N23}$$

$$RR2 = \frac{N12}{N22} \bigg/ \frac{N11 + N13}{N21 + N23}$$

$$RR3 = \frac{N13}{N23} \bigg/ \frac{N11 + N12}{N21 + N22}$$

- Here, the *case* and *control* populations represent any case-control-group pair, or bad(case)-good(control)-group pair, respectively (due to their increased response to statins, 'high responders' are treated as a case cohort, whereas 'low responders' are treated as the respective control cohort). A value $RR1 > 1$, $RR2 > 1$, and $RR3 > 1$ indicates an increased risk for individuals carrying genotype 1, genotype 2, and genotype 3, respectively. For example, $RR1 = 3$ indicates a 3-fold risk of an individual carrying genotype 1 as compared to individuals carrying genotype 2 or 3 (a detailed description of relative risk calculation and statistics can be found in (Biostatistics, L. D. Fisher and G. van Belle, Wiley Interscience 1993)). The baySNP number refers to an internal numbering of the PA SNPs and can be found in the sequence listing. null: not defined.

In cases where a relative risk is not given in the table (three times zero or null) the informative genotype can be drawn from the right part of the table where the frequencies of genotypes are given in the cases and control cohorts. For example BaySNP 3360 gave the following results:

5

BAYSNP	COMPARISON	CTYPE1	CTYPE2	CTYPE3	RR1	RR2	RR3
3360	HELD_MAL_ADR5ULN	GG	GT	TT	null	0	0

FQ1_A	FQ2_A	FQ3_A	FQ1_B	FQ2_B	FQ3_B
10	0	0	50	22	1

It can be concluded that a GT or TT genotype is only present in the control cohort; these genotypes are somehow protective against ADR. An analogous proceeding can be used to determine protective alleles if no relative risk is given (table 6b).

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DAVSNR	ALLELE1	ALLELE2	COMPARISON	RR	RR2	SIZE A	FREQ A	FREQ A PRG	SIZE B	FREQ B	RR2 B
29	A	G	HELD_FEM_LIP	1,26	0,79	80	100	60	78	80	76
29	A	G	HELD_ALL_ADR3ULN	1,33	0,75	47	54	40	131	125	137
29	A	G	HELD_ALL_LIP	1,23	0,81	99	122	76	114	119	109
52	C	G	HELD_ALL_CC	0,63	1,6	43	42	44	39	57	21
52	C	G	HELD_MAL_HDL	0,94	1,06	18	20	16	25	29	21
52	C	G	HELD_FEM_CC	0,69	1,45	29	27	31	22	30	14
52	C	G	HELD_MAL_CC	0,55	1,82	14	15	13	17	27	7
52	C	G	HELD_MAL_LIP2	0,88	1,14	253	254	252	281	317	245
57	C	T	HELD_FEM_CC	0,62	1,62	31	45	17	22	41	3
118	C	T	HELD_MAL_LIP2	1,16	0,86	306	493	119	337	512	162
137	G	A	HELD_MAL_ADR5ULN	0,46	2,18	8	7	9	54	71	37
137	G	A	HELD_ALL_ADR5ULN	0,73	1,37	23	25	21	119	151	87
137	G	A	HELD_ALL_ADR3ULN	0,72	1,39	44	46	42	119	151	87
179	G	A	HELD_MAL_ADR5ULN	1,07	0,93	8	14	2	56	97	15
179	G	A	HELD_MAL_ADR3ULN	1,38	0,72	16	29	3	56	97	15
179	G	A	HELD_ALL_ADR5ULN	1,16	0,86	25	45	5	124	219	29
179	G	A	HELD_ALL_ADR	1,2	0,84	128	234	22	124	219	29
240	G	C	HELD_ALL_ADR3ULN	2,22	0,45	44	83	5	130	224	36
240	G	C	HELD_MAL_ADR3ULN	4,16	0,24	17	33	1	59	102	16
241	G	A	HELD_ALL_ADR3ULN	0,66	1,51	47	60	34	129	196	62
241	G	A	HELD_ALL_ADR5ULN	0,58	1,72	25	31	19	129	196	62
241	G	A	HELD_MAL_ADR3ULN	0,54	1,84	17	19	15	58	86	30

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE A	FREQ A	FREQ	SIZE B	FREQ B	FREQ2 B
288	G	C	CVD_ALL	0,82	1,22	101	146	56	73	119	27
384	C	G	CVD_ALL	1,13	0,89	104	123	85	74	77	71
384	C	G	HELD_FEM_CC	1,47	0,68	31	38	24	22	17	27
533	G	A	CVD_ALL	0,8	1,25	103	162	44	74	129	19
542	G	A	HELD_FEM_ADR	0,78	1,28	73	118	28	71	125	17
576	C	T	HELD_ALL_LIP	null	0	100	200	0	115	225	5
576	C	T	HELD_FEM_LIP	null	0	81	162	0	79	154	4
608	G	A	CVD_MAL	1,57	0,64	68	120	16	33	47	19
614	G	A	HELD_MAL_HDL	6,2	0,16	20	30	10	26	0	52
614	G	A	HELD_ALL_CC	0,65	1,53	44	57	31	40	67	13
614	G	A	HELD_MAL_CC	0,47	2,12	13	12	14	18	28	8
614	G	A	HELD_MAL_LIP	0,52	1,92	19	21	17	35	55	15
614	G	A	CVD_ALL	0,8	1,25	96	126	66	63	98	28
614	G	A	HELD_FEM_CC	0,69	1,44	31	45	17	22	39	5
738	A	C	CVD_ALL	0,82	1,22	104	106	102	74	93	55
1056	A	G	HELD_ALL_HDL	1,58	0,63	34	51	17	50	59	41
1056	A	G	HELD_FEM_LIP	0,81	1,24	78	98	58	78	113	43
1092	G	C	HELD_MAL_ADR5ULN	1,28	0,78	8	12	4	59	82	36
1524	C	A	HELD_MAL_CC2	0,7	1,43	44	56	32	26	44	8
1524	C	A	HELD_ALL_LIP	1,28	0,78	96	151	41	112	158	66
1524	C	A	HELD_ALL_CC	1,52	0,66	44	72	16	39	52	26
1574	T	C	CVD_MAL	1,15	0,87	69	119	19	34	55	13

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE A	FRQ1 A	FRQ2 A	FRQ1 B	SIZE B	FRQ1 B	FRQ2 B
1582	T	C	HELD_MAL_ADR3ULN	3,32	0,3	16	30	2	53	83	23	
1657	C	T	HELD_FEM_EFF	1,19	0,84	23	29	17	33	37	29	
1722	T	C	CVD_MAL	1,1	0,91	63	79	47	33	37	29	
1756	C	T	HELD_MAL_ADR5ULN	0,36	2,81	9	14	4	56	104	8	
1757	G	A	HELD_ALL_CC	0,87	1,15	45	63	27	38	58	18	
1757	G	A	HELD_FEM_CC	0,77	1,3	31	40	22	21	33	9	
1757	G	A	HELD_FEM_VEFF	0,84	1,19	148	177	119	152	206	98	
1757	G	A	HELD_MAL_ADR	0,94	1,06	62	90	34	58	87	29	
1765	A	G	HELD_ALL_LIP	0,86	1,16	100	29	171	107	39	175	
1767	T	C	HELD_ALL_ADR3ULN	2,85	0,35	40	75	5	107	172	42	
1767	T	C	HELD_ALL_ADR5ULN	4,15	0,24	21	40	2	107	172	42	
1767	T	C	HELD_MAL_ADR5ULN	0	null	7	0	14	53	86	20	
1767	T	C	HELD_FEM_ADR3ULN	2,39	0,42	27	50	4	54	86	22	
1767	T	C	HELD_MAL_ADR3ULN	4,73	0,21	13	25	1	53	86	20	
1837	C	T	HELD_ALL_ADR3ULN	1,61	0,62	48	75	21	132	173	91	
1837	C	T	HELD_FEM_LIP	1,14	0,88	81	120	42	79	109	49	
1837	C	T	HELD_ALL_LIP	1,11	0,9	100	145	55	115	158	72	
1837	C	T	HELD_ALL_ADR	1,19	0,84	134	195	73	132	173	91	
1854	A	G	HELD_FEM_LIP	0,81	1,23	80	85	75	79	100	58	
1862	C	T	HELD_FEM_LIP	1,34	0,75	80	121	39	76	97	55	
2085	G	T	HELD_FEM_CC	1,6	0,62	31	44	18	22	20	24	
2085	G	T	HELD_ALL_CC	1,44	0,7	45	61	29	40	40	40	

SNP	ALLELE1	ALLELE2	COMPARISON	RR	RR1	RR2	SIZE	TRIO1 A	TRIO1 B	TRIO2 A	TRIO2 B	SIZE	TRIO1 A	TRIO1 B	TRIO2 A	TRIO2 B
2093	C	T	HELD_MAL_CC	0,42	2,4		14	15		13		18	32		18	4
2093	C	T	HELD_ALL_CC	0,73	1,38		45	62		28		40	66		40	14
2109	A	G	HELD_MAL_HDL	2,22	0,45		19	34		4		22	31		22	13
2109	A	G	HELD_ALL_HDL	1,68	0,6		39	70		8		48	76		48	20
2109	A	G	HELD_ALL_LIP2	1,14	0,88		624	1035		213		700	1109		700	291
2109	A	G	HELD_FEM_LIP	1,46	0,69		80	139		21		78	120		78	36
2124	G	T	HELD_MAL_LIP	0,57	1,75		17	14		20		32	40		32	24
2140	G	T	HELD_FEM_UEFF	2,15	0,46		43	79		7		60	94		60	26
2140	G	T	HELD_FEM_EFF	1,3	0,77		237	416		58		239	390		239	88
2140	G	T	HELD_MAL_ADR	1,61	0,62		46	80		12		49	73		49	25
2140	G	T	HELD_FEM_VEFF	1,35	0,74		119	207		31		122	194		122	50
2141	G	A	HELD_MAL_ADR3ULN	3,89	0,26		16	30		2		52	78		52	26
2141	G	A	HELD_FEM_UEFF	1,37	0,73		53	91		15		77	121		77	33
2141	G	A	HELD_MAL_ADR	1,47	0,68		58	100		16		52	78		52	26
2186	T	C	HELD_MAL_ADR3ULN	0,37	2,7		9	14		4		59	109		59	9
2187	C	T	HELD_FEM_ADR3ULN	0,65	1,54		30	37		23		71	107		71	35
2192	G	A	HELD_FEM_ADR	7,27	0,14		69	137		1		70	127		70	13
2192	G	A	HELD_FEM_ADR3ULN	0	null		30	0		60		70	127		70	13
2192	G	A	HELD_ALL_ADR	2,19	0,46		132	258		6		126	233		126	19
2192	G	A	HELD_FEM_ADR3ULN	0	null		16	0		32		70	127		70	13
2192	G	A	HELD_ALL_ADR3ULN	2,97	0,34		47	92		2		126	233		126	19
2203	T	C	HELD_FEM_LIP	0,74	1,35		80	106		54		79	125		79	33

FRAYSNP	ALLELE1	ALLELE2	COMPARISON	HR1	HR2	SIZE A	FRQ A	FRQ A	FRQ A	FRQ B	FRQ B	FRQ B
2203	T	C	HELD_ALL_LIP	0,8	1,25	98	128	68	115	171	59	59
2217	G	T	HELD_MAL_CC	0,46	2,17	13	14	12	17	29	5	5
2217	G	T	CVD_FEM	2,4	0,42	33	63	3	40	68	12	12
2281	A	C	HELD_FEM_CC	0,64	1,55	31	26	36	22	30	14	14
2281	A	C	HELD_MAL_CC	1,71	0,58	14	20	8	18	18	18	18
2284	G	A	HELD_MAL_LIP	3,58	0,28	17	32	2	35	53	17	17
2290	A	G	HELD_MAL_CC	0,42	2,41	14	18	10	18	34	2	2
2327	A	C	HELD_MAL_ADR	1,24	0,8	59	70	48	54	52	56	56
2327	A	C	HELD_MAL_ADR5ULN	1,57	0,64	9	11	7	54	52	56	56
2327	A	C	HELD_MAL_ADR3ULN	1,68	0,59	17	22	12	54	52	56	56
2327	A	C	HELD_FEM_BFF	0,9	1,11	270	249	291	281	287	275	275
2353	A	G	CVD_MAL	0,74	1,36	66	117	15	21	42	0	0
2353	A	G	HELD_ALL_CC	1,62	0,62	45	83	7	38	63	13	13
2353	A	G	CVD_ALL	0,77	1,29	100	178	22	49	94	4	4
2353	A	G	HELD_FEM_CC	1,54	0,65	31	58	4	21	36	6	6
2371	A	C	HELD_ALL_LIP2	0,91	1,1	630	927	333	726	1117	335	335
2376	C	T	HELD_ALL_LIP2	0,79	1,26	620	1193	47	717	1400	34	34
2401	T	G	HELD_FEM_URFF	0,77	1,31	52	76	28	73	119	27	27
2463	T	C	HELD_ALL_CC	11,29	0,09	44	81	7	36	0	72	72
2463	T	C	HELD_FEM_CC	8,33	0,12	30	54	6	22	0	44	44
2463	T	C	HELD_FEM_LIP2	0,96	1,04	307	572	42	370	693	47	47
2755	A	G	HELD_FEM_ADR	0,77	1,31	72	69	75	70	86	54	54

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR	RR2	SIZE	FRQ1	FRQ2	SIZE	FRQ1	FRQ2	FRQ1	FRQ2
2755	A	G	HELD_ALL_ADR	0,85	1,18	134	147	121	128	162	94		
2755	A	G	HELD_FEM_EFF	1,05	0,95	271	331	211	284	333	235		
2925	G	A	HELD_FEM_VEFF	1,27	0,79	141	163	119	145	134	156		
2925	G	A	HELD_FEM_UEFF	1,48	0,68	54	64	44	77	66	88		
3043	G	A	HELD_FEM_ADR3ULN	2,96	0,34	17	32	2	31	49	13		
3152	T	A	HELD_FEM_VEFF	1,1	0,91	107	125	89	108	116	100		
3214	C	G	HELD_FEM_VEFF	1,09	0,92	151	253	49	142	231	53		
3215	C	G	HELD_MAL_ADR5ULN	0,12	8,06	9	17	1	60	120	0		
3237	C	G	HELD_FEM_CC	3,84	0,26	28	55	1	18	31	5		
3241	T	C	HELD_MAL_ADR	1,4	0,71	45	57	33	51	49	53		
3826	C	A	HELD_MAL_ADR5ULN	0	null	7	0	14	44	71	17		
3826	C	A	HELD_ALL_ADR5ULN	4,58	0,22	18	35	1	90	156	24		
3826	C	A	HELD_MAL_ADR3ULN	4,4	0,23	12	23	1	44	71	17		
3842	C	G	CVD_ALL	0,6	1,66	100	190	10	63	126	0		
3842	C	G	CVD_MAL	0,68	1,47	68	129	7	30	60	0		
3842	C	G	CVD_FEM	0,48	2,08	32	61	3	33	66	0		
3843	A	T	HELD_MAL_CC2	1,45	0,69	23	32	14	17	17	17		
3843	A	T	HELD_FEM_HDL	0,63	1,59	12	11	13	15	20	10		
3869	G	T	HELD_FEM_UEFF	1,46	0,69	53	76	30	73	84	62		
3942	C	A	HELD_FEM_VEFF	0,55	1,81	54	91	17	74	141	7		
4018	T	C	HELD_MAL_LIP	2,11	0,47	18	30	6	36	46	26		
4206	A	T	HELD_ALL_ADR3ULN	0,7	1,43	48	47	49	132	161	103		

CHASNP	ALLELE1	ALLELE2	COMPARISON	RR	REF. SIZE	HTOI_A	HTOI_A	HTOI_A	HTOI_A	HTOI_B	HTOI_B	HTOI_B	HTOI_B
4206	A	T	HELD_FEM_ADR	0,79	1,27	72	72	72	72	72	89	89	55
4206	A	T	HELD_ALL_ADR5ULN	0,61	1,65	26	24	28	28	132	161	161	103
4527	G	A	CVD_ALL	1,18	0,85	71	114	28	28	54	80	80	28
4527	G	A	HELD_FEM_LIP2	1,19	0,84	320	508	132	132	370	546	546	194
4527	G	A	HELD_MAL_CC	0,47	2,15	12	17	7	7	16	30	30	2
4527	G	A	HELD_MAL_CC2	1,43	0,7	45	71	19	19	29	36	36	22
4527	G	A	HELD_ALL_ADR3ULN	0,67	1,5	48	68	28	28	124	202	202	46
4527	G	A	HELD_ALL_CC2	1,24	0,81	104	162	46	46	71	97	97	45
4527	G	A	HELD_ALL_ADR5ULN	0,59	1,71	26	36	16	16	124	202	202	46
4544	G	A	HELD_MAL_ADR3ULN	0,43	2,34	17	20	14	14	59	97	97	21
4544	G	A	HELD_MAL_ADR	0,74	1,35	62	87	37	37	59	97	97	21
4544	G	A	HELD_ALL_ADR	0,82	1,23	133	183	83	83	130	201	201	59
4544	G	A	HELD_ALL_ADR3ULN	0,69	1,44	47	63	31	31	130	201	201	59
4545	G	A	HELD_MAL_ADR3ULN	0,43	2,34	17	20	14	14	59	97	97	21
4545	G	A	HELD_MAL_ADR	0,73	1,37	61	85	37	37	59	97	97	21
4545	G	A	HELD_ALL_ADR	0,82	1,22	132	181	83	83	128	197	197	59
4668	C	A	HELD_ALL_ADR5ULN	1,52	0,66	26	34	18	18	130	139	139	121
4669	C	T	HELD_FEM_EFF	0,85	1,17	286	474	98	98	281	490	490	72
4718	G	A	HELD_MAL_LIP	1,44	0,7	18	26	10	10	34	41	41	27
4818	G	A	HELD_MAL_LIP	0,62	1,62	17	20	14	14	36	54	54	18
4827	A	G	HELD_MAL_ADR5ULN	0,76	1,31	9	15	3	3	59	103	103	15
4838	A	G	HELD_ALL_CC2	1,2	0,83	101	113	89	89	71	64	64	78

BAYSNP	ALLELE1	ALLELE2	COMPARISON	PRO_RR	SIZE_A	FREQ_A	FREQ_A	SIZE_B	FREQ_B	FREQ_B
4856	G	A	CVD_MAL	0	null	69	0	138	34	65
4868	T	C	HELD_MAL_ADR	0,84	1,19	62	88	36	59	92
4868	T	C	HELD_MAL_ADR5ULN	0,66	1,51	8	11	5	59	92
4887	C	A	HELD_MAL_CC	3,98	0,25	14	26	2	18	23
4887	C	A	HELD_ALL_CC	1,48	0,67	45	75	15	38	53
4912	G	A	HELD_MAL_LIP	0,45	2,21	12	7	17	31	34
4951	G	A	HELD_ALL_ADR3ULN	0,9	1,11	48	51	45	128	145
4951	G	A	HELD_FEM_ADR3ULN	0,78	1,28	31	29	33	69	77
4951	G	A	HELD_FEM_ADR5ULN	0,56	1,77	17	13	21	69	77
4951	G	A	HELD_ALL_ADR5ULN	0,62	1,62	26	22	30	128	145
4951	G	A	HELD_FEM_ADR	0,84	1,2	73	68	78	69	77
4951	G	A	HELD_ALL_ADR	0,88	1,14	135	135	135	128	145
4952	T	C	HELD_ALL_ADR3ULN	0,93	1,08	48	52	44	128	145
4952	T	C	HELD_FEM_ADR3ULN	0,78	1,28	31	30	32	70	80
4952	T	C	HELD_FEM_ADR5ULN	0,6	1,68	17	14	20	70	80
4952	T	C	HELD_ALL_ADR5ULN	0,66	1,51	26	23	29	128	145
4966	G	A	HELD_MAL_LIP	2,11	0,47	18	27	9	34	34
4966	G	A	HELD_MAL_ADR	1,24	0,81	61	68	54	59	53
4966	G	A	HELD_FEM_CC	0,71	1,4	30	25	35	21	26
5019	A	T	CVD_FEM	0,6	1,66	32	25	39	34	43
5019	A	T	HELD_ALL_CC2	1,21	0,82	87	96	78	62	54
5019	A	T	HELD_MAL_HDL	2,11	0,47	18	27	9	22	20

DATA NP	ALLELE1	ALLELE2	COMPARISON	IR	REL	SIZE A	FRQ A	FRQ A SIZE	FRQ B	FRQ B SIZE	FRQ B
5019	A	T	HELD_ALL_LIP	1,33	0,75	86	95	77	100	84	116
5019	A	T	HELD_MAL_CC2	1,43	0,7	37	43	31	24	17	31
5165	C	A	HELD_FEM_ADR5ULN	0,63	1,6	30	46	14	70	122	18
5165	C	A	HELD_MAL_ADR5ULN	0,76	1,31	9	15	3	59	103	15
5165	C	A	HELD_FEM_ADR	0,82	1,21	71	116	26	70	122	18
5165	C	A	HELD_FEM_ADR5ULN	0,53	1,87	16	24	8	70	122	18
5278	G	A	HELD_MAL_ADR5ULN	0,42	2,35	9	10	8	60	93	27
5287	C	T	HELD_FEM_VEFF	0,77	1,29	159	257	61	147	260	34
5320	A	G	CVD_FEM	1,5	0,67	33	40	26	38	32	44
5324	T	C	HELD_FEM_VEFF	0,83	1,2	137	124	150	134	146	122
5373	G	T	HELD_FEM_ADR5ULN	4,01	0,25	16	29	3	71	94	48
5373	G	T	HELD_ALL_ADR5ULN	2,13	0,47	25	42	8	131	180	82
5375	C	T	HELD_FEM_ADR5ULN	4,08	0,25	15	27	3	70	90	50
5375	C	T	HELD_ALL_ADR5ULN	1,88	0,53	24	39	9	128	173	83
5376	A	T	HELD_MAL_ADR5ULN	0,11	8,73	8	15	1	58	116	0
5377	T	C	HELD_FEM_ADR	1,19	0,84	60	88	32	64	85	43
5377	T	C	HELD_FEM_ADR5ULN	2,75	0,36	15	26	4	64	85	43
5517	A	G	HELD_MAL_ADR	1,49	0,67	53	104	2	55	106	4
5518	G	C	HELD_FEM_ADR5ULN	143	0,01	16	31	1	71	0	142
5564	G	T	CVD_MAL	0,85	1,17	69	73	65	34	44	24
5569	G	A	HELD_MAL_ADR5ULN	5,56	0,18	8	15	1	53	74	32
5569	G	A	HELD_ALL_ADR5ULN	2,07	0,48	22	37	7	122	170	74

REFSNP	ALLELE1	ALLELE2	COMPARISON	RR	RR2	SIZE	FREQ1_A	FREQ2_A	SIZE_B	FREQ1_B	FREQ2_B
5716	G	C	HELD_ALL_ADR3ULN	0,57	1,74	44	34	54	109	126	92
5716	G	C	HELD_FEM_ADR3ULN	0,5	1,98	29	18	40	59	65	53
5716	G	C	HELD_ALL_ADR5ULN	0,48	2,07	22	16	28	109	126	92
5716	G	C	HELD_FEM_ADR5ULN	0,49	2,05	15	10	20	59	65	53
5717	G	A	HELD_ALL_ADR5ULN	0,59	1,68	26	20	32	132	142	122
5717	G	A	CVD_FEM	0,61	1,64	17	12	22	19	22	16
5850	G	A	HELD_MAL_CC	0,66	1,52	14	14	14	15	21	9
5959	G	A	CVD_MAL	1,25	0,8	58	78	38	29	30	28
6151	C	A	HELD_MAL_ADR	0,87	1,15	58	76	40	58	83	33
6236	T	C	HELD_ALL_ADR	0,85	1,18	129	177	81	128	193	63
6277	T	G	HELD_FEM_ADR5ULN	0,44	2,25	16	21	11	66	112	20
6277	T	G	HELD_ALL_ADR5ULN	0,6	1,67	23	33	13	124	205	43
6277	T	G	HELD_FEM_ADR	0,73	1,37	72	105	39	66	112	20
6277	T	G	HELD_FEM_ADR3ULN	0,58	1,74	30	42	18	66	112	20
6313	C	T	HELD_FEM_UEFF	0,79	1,26	52	54	50	72	89	55
6369	T	C	HELD_FEM_LIP	1,31	0,77	63	82	44	68	72	64
6374	T	C	HELD_ALL_ADR3ULN	0,63	1,58	47	52	42	126	177	75
6374	T	C	HELD_MAL_ADR3ULN	0,47	2,13	17	15	19	58	79	37
6396	T	C	HELD_MAL_CC	0	null	14	0	28	18	30	6
6396	T	C	HELD_ALL_CC	1,76	0,57	45	83	7	40	65	15
6396	T	C	CVD_FEM	0,66	1,51	35	55	15	37	67	7
6396	T	C	CVD_ALL	0,77	1,3	97	167	27	70	130	10

RAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE A	FRQ1 A	FRQ1 B	FRQ2 A	FRQ2 B	SIZE A	FRQ1 A	FRQ1 B	FRQ2 A	FRQ2 B
7363	G	A	HELD_ALL_LIP	0,78	1,28	100	143	57	115	185	45				
7409	A	G	HELD_FEM_ADR5ULN	0,37	2,67	17	24	10	72	130	14				
7409	A	G	HELD_FEM_ADR3ULN	0,54	1,85	31	48	14	72	130	14				
7409	A	G	HELD_MAL_ADR5ULN	null	0	7	14	0	59	95	23				
8138	T	C	HELD_MAL_LIP	2,16	0,46	19	28	10	35	33	37				
8138	T	C	HELD_MAL_OC	1,25	0,8	14	16	12	19	18	20				
8138	T	C	HELD_ALL_LIP	1,22	0,82	94	112	76	114	116	112				
8168	C	A	HELD_MAL_LIP	0,48	2,1	19	28	10	36	66	6				
8168	C	A	HELD_FEM_LIP	1,3	0,77	79	136	22	79	125	33				
8210	G	A	HELD_ALL_ADR3ULN	0,95	1,05	46	53	39	124	147	101				
8210	G	A	HELD_FEM_ADR3ULN	0,83	1,2	29	30	28	67	78	56				
8210	G	A	HELD_FEM_ADR	0,86	1,16	69	70	68	67	78	56				
8210	G	A	HELD_ALL_ADR	0,9	1,11	127	137	117	124	147	101				
8241	A	G	HELD_FEM_LIP	1,66	0,6	76	136	16	77	120	34				
8241	A	G	HELD_ALL_LIP	1,38	0,72	95	166	24	112	179	45				
8249	C	T	HELD_ALL_ADR3ULN	0,57	1,75	48	86	10	129	246	12				
8249	C	T	HELD_ALL_ADR5ULN	0,47	2,12	26	46	6	129	246	12				
8480	C	G	CVD_FEM	0,38	2,63	27	48	6	39	78	0				
8480	C	G	CVD_MAL	0,59	1,69	54	99	9	34	68	0				
8577	T	C	HELD_ALL_ADR3ULN	0,68	1,48	47	50	44	126	167	85				
8577	T	C	HELD_ALL_ADR	0,83	1,2	132	151	113	126	167	85				
8577	T	C	HELD_ALL_ADR5ULN	0,61	1,63	26	27	25	126	167	85				

BAYSNP	AEFFLE1	ALLELE1	COMPARISON	REF. SIZE	FR01	FR02	SIZE	FR01	FR02	SIZE	FR01	FR02	SIZE	FR01	FR02	SIZE	FR01	FR02	SIZE
8578	G	A	HELD_ALL_ADR3ULN	0,7	1,43	48	51	45	130	169	91								
8653	C	T	HELD_MAL_ADR	2,22	0,45	47	87	7	52	81	23								
8653	C	T	HELD_MAL_ADR3ULN	6	0,17	14	27	1	52	81	23								
8653	C	T	HELD_MAL_ADR5ULN	mm	0	7	14	0	52	81	23								
8653	C	T	HELD_ALL_ADR3ULN	1,74	0,58	41	74	8	114	187	41								
8816	G	C	HELD_FEM_LIP2	1,18	0,84	315	403	227	370	419	321								
8816	G	C	HELD_FEM_HDL	1,9	0,53	18	24	12	22	17	27								
8816	G	C	HELD_ALL_CC2	1,25	0,8	90	121	59	70	78	62								
8816	G	C	CVD_ALL	0,78	1,28	92	138	46	65	111	19								
8816	G	C	HELD_FEM_CC2	1,37	0,73	52	71	33	42	44	40								
8816	G	C	HELD_MAL_HDL	0,99	1,01	18	22	14	17	21	13								
8931	C	T	HELD_FEM_ADR3ULN	2,16	0,46	23	43	3	42	70	14								
8943	A	C	HELD_MAL_ADR3ULN	3,52	0,28	16	30	2	55	85	25								
9243	C	G	HELD_FEM_VBEFF	1,17	0,85	139	230	48	143	223	63								
9243	C	G	HELD_MAL_ADR5ULN	2,32	0,43	9	16	2	60	91	29								
9243	C	G	HELD_FEM_UBEFF	1,31	0,77	54	90	18	74	113	35								
9523	G	A	HELD_MAL_ADR5ULN	0,37	2,69	8	12	4	60	109	11								
9940	C	T	HELD_MAL_CC	mm	0	12	24	0	14	23	5								
9940	C	T	HELD_ALL_CC	2	0,5	38	71	5	31	50	12								
10091	T	C	HELD_ALL_ADR3ULN	0,66	1,52	48	74	22	129	222	36								
10541	G	C	HELD_FEM_UBEFF	1,89	0,53	55	103	7	77	131	23								
10541	G	C	HELD_FEM_VBEFF	1,46	0,68	151	283	19	145	256	34								

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR	RR2	SIZE A	FREQ1 A	FREQ2 A	SIZE B	FREQ1 B	FREQ2 B
10600	G	A	CVD_MAL	0	null	67	0	134	34	64	4
10600	G	A	HELD_ALL_HDL	0	null	39	0	78	47	88	6
10600	G	A	HELD_MAL_HDL	0	null	19	0	38	23	42	4
10745	G	A	HELD_MAL_LIP	1,96	0,51	19	32	6	35	47	23
10748	T	C	HELD_MAL_LIP	0,53	1,89	13	15	11	30	47	13
10749	C	G	HELD_FEM_LIP	1,34	0,75	81	124	38	77	100	54
10785	T	C	CVD_MAL	1,47	0,68	69	128	10	33	55	11
10811	A	G	HELD_FEM_LIP2	1,18	0,85	243	382	104	300	440	160
10811	A	G	CVD_ALL	0,82	1,22	103	155	51	74	124	24
10830	G	A	HELD_ALL_LIP2	1,13	0,89	637	723	551	725	742	708
10830	G	A	HELD_ALL_LIP	1,35	0,74	99	113	85	114	98	130
10830	G	A	HELD_MAL_LIP2	1,16	0,86	314	357	271	347	346	348
10830	G	A	CVD_FEM	1,56	0,64	35	44	26	39	33	45
10830	G	A	HELD_MAL_LIP	1,84	0,54	19	24	14	36	29	43
10830	G	A	HELD_FEM_LIP	1,25	0,8	80	89	71	78	69	87
10949	G	C	HELD_FEM_VEFF	0,83	1,2	140	163	117	143	191	95
10949	G	C	HELD_FEM_BFF	0,88	1,14	269	319	219	282	369	195
10962	A	G	CVD_FEM	0,33	3,07	18	2	34	18	9	27
10962	A	G	HELD_ALL_ADR3ULN	1,27	0,79	47	75	19	117	173	61
10966	T	C	HELD_ALL_ADR3ULN	1,36	0,74	47	74	20	126	179	73
10966	T	C	HELD_ALL_ADR5ULN	1,92	0,52	25	42	8	126	179	73
11000	T	C	HELD_MAL_LIP2	1,19	0,84	313	483	143	348	495	201

BACT	ALLELE1	ALLELE2	COMPARISON	RM	RM2	RM3	RM4	RM5	RM6	RM7	RM8	RM9	RM10	RM11	RM12	RM13	RM14	RM15	RM16	RM17	RM18	RM19	RM20	RM21	RM22	RM23	RM24	RM25	RM26	RM27	RM28	RM29	RM30	RM31	RM32	RM33	RM34	RM35	RM36	RM37	RM38	RM39	RM40	RM41	RM42	RM43	RM44	RM45	RM46	RM47	RM48	RM49	RM50	RM51	RM52	RM53	RM54	RM55	RM56	RM57	RM58	RM59	RM60	RM61	RM62	RM63	RM64	RM65	RM66	RM67	RM68	RM69	RM70	RM71	RM72	RM73	RM74	RM75	RM76	RM77	RM78	RM79	RM80	RM81	RM82	RM83	RM84	RM85	RM86	RM87	RM88	RM89	RM90	RM91	RM92	RM93	RM94	RM95	RM96	RM97	RM98	RM99	RM100	RM101	RM102	RM103	RM104	RM105	RM106	RM107	RM108	RM109	RM110	RM111	RM112	RM113	RM114	RM115	RM116	RM117	RM118	RM119	RM120	RM121	RM122	RM123	RM124	RM125	RM126	RM127	RM128	RM129	RM130	RM131	RM132	RM133	RM134	RM135	RM136	RM137	RM138	RM139	RM140	RM141	RM142	RM143	RM144	RM145	RM146	RM147	RM148	RM149	RM150	RM151	RM152	RM153	RM154	RM155	RM156	RM157	RM158	RM159	RM160	RM161	RM162	RM163	RM164	RM165	RM166	RM167	RM168	RM169	RM170	RM171	RM172	RM173	RM174	RM175	RM176	RM177	RM178	RM179	RM180	RM181	RM182	RM183	RM184	RM185	RM186	RM187	RM188	RM189	RM190	RM191	RM192	RM193	RM194	RM195	RM196	RM197	RM198	RM199	RM200	RM201	RM202	RM203	RM204	RM205	RM206	RM207	RM208	RM209	RM210	RM211	RM212	RM213	RM214	RM215	RM216	RM217	RM218	RM219	RM220	RM221	RM222	RM223	RM224	RM225	RM226	RM227	RM228	RM229	RM230	RM231	RM232	RM233	RM234	RM235	RM236	RM237	RM238	RM239	RM240	RM241	RM242	RM243	RM244	RM245	RM246	RM247	RM248	RM249	RM250	RM251	RM252	RM253	RM254	RM255	RM256	RM257	RM258	RM259	RM260	RM261	RM262	RM263	RM264	RM265	RM266	RM267	RM268	RM269	RM270	RM271	RM272	RM273	RM274	RM275	RM276	RM277	RM278	RM279	RM280	RM281	RM282	RM283	RM284	RM285	RM286	RM287	RM288	RM289	RM290	RM291	RM292	RM293	RM294	RM295	RM296	RM297	RM298	RM299	RM300	RM301	RM302	RM303	RM304	RM305	RM306	RM307	RM308	RM309	RM310	RM311	RM312	RM313	RM314	RM315	RM316	RM317	RM318	RM319	RM320	RM321	RM322	RM323	RM324	RM325	RM326	RM327	RM328	RM329	RM330	RM331	RM332	RM333	RM334	RM335	RM336	RM337	RM338	RM339	RM340	RM341	RM342	RM343	RM344	RM345	RM346	RM347	RM348	RM349	RM350	RM351	RM352	RM353	RM354	RM355	RM356	RM357	RM358	RM359	RM360	RM361	RM362	RM363	RM364	RM365	RM366	RM367	RM368	RM369	RM370	RM371	RM372	RM373	RM374	RM375	RM376	RM377	RM378	RM379	RM380	RM381	RM382	RM383	RM384	RM385	RM386	RM387	RM388	RM389	RM390	RM391	RM392	RM393	RM394	RM395	RM396	RM397	RM398	RM399	RM400	RM401	RM402	RM403	RM404	RM405	RM406	RM407	RM408	RM409	RM410	RM411	RM412	RM413	RM414	RM415	RM416	RM417	RM418	RM419	RM420	RM421	RM422	RM423	RM424	RM425	RM426	RM427	RM428	RM429	RM430	RM431	RM432	RM433	RM434	RM435	RM436	RM437	RM438	RM439	RM440	RM441	RM442	RM443	RM444	RM445	RM446	RM447	RM448	RM449	RM450	RM451	RM452	RM453	RM454	RM455	RM456	RM457	RM458	RM459	RM460	RM461	RM462	RM463	RM464	RM465	RM466	RM467	RM468	RM469	RM470	RM471	RM472	RM473	RM474	RM475	RM476	RM477	RM478	RM479	RM480	RM481	RM482	RM483	RM484	RM485	RM486	RM487	RM488	RM489	RM490	RM491	RM492	RM493	RM494	RM495	RM496	RM497	RM498	RM499	RM500	RM501	RM502	RM503	RM504	RM505	RM506	RM507	RM508	RM509	RM510	RM511	RM512	RM513	RM514	RM515	RM516	RM517	RM518	RM519	RM520	RM521	RM522	RM523	RM524	RM525	RM526	RM527	RM528	RM529	RM530	RM531	RM532	RM533	RM534	RM535	RM536	RM537	RM538	RM539	RM540	RM541	RM542	RM543	RM544	RM545	RM546	RM547	RM548	RM549	RM550	RM551	RM552	RM553	RM554	RM555	RM556	RM557	RM558	RM559	RM560	RM561	RM562	RM563	RM564	RM565	RM566	RM567	RM568	RM569	RM570	RM571	RM572	RM573	RM574	RM575	RM576	RM577	RM578	RM579	RM580	RM581	RM582	RM583	RM584	RM585	RM586	RM587	RM588	RM589	RM590	RM591	RM592	RM593	RM594	RM595	RM596	RM597	RM598	RM599	RM600	RM601	RM602	RM603	RM604	RM605	RM606	RM607	RM608	RM609	RM610	RM611	RM612	RM613	RM614	RM615	RM616	RM617	RM618	RM619	RM620	RM621	RM622	RM623	RM624	RM625	RM626	RM627	RM628	RM629	RM630	RM631	RM632	RM633	RM634	RM635	RM636	RM637	RM638	RM639	RM640	RM641	RM642	RM643	RM644	RM645	RM646	RM647	RM648	RM649	RM650	RM651	RM652	RM653	RM654	RM655	RM656	RM657	RM658	RM659	RM660	RM661	RM662	RM663	RM664	RM665	RM666	RM667	RM668	RM669	RM670	RM671	RM672	RM673	RM674	RM675	RM676	RM677	RM678	RM679	RM680	RM681	RM682	RM683	RM684	RM685	RM686	RM687	RM688	RM689	RM690	RM691	RM692	RM693	RM694	RM695	RM696	RM697	RM698	RM699	RM700	RM701	RM702	RM703	RM704	RM705	RM706	RM707	RM708	RM709	RM710	RM711	RM712	RM713	RM714	RM715	RM716	RM717	RM718	RM719	RM720	RM721	RM722	RM723	RM724	RM725	RM726	RM727	RM728	RM729	RM730	RM731	RM732	RM733	RM734	RM735	RM736	RM737	RM738	RM739	RM740	RM741	RM742	RM743	RM744	RM745	RM746	RM747	RM748	RM749	RM750	RM751	RM752	RM753	RM754	RM755	RM756	RM757	RM758	RM759	RM760	RM761	RM762	RM763	RM764	RM765	RM766	RM767	RM768	RM769	RM770	RM771	RM772	RM773	RM774	RM775	RM776	RM777	RM778	RM779	RM780	RM781	RM782	RM783	RM784	RM785	RM786	RM787	RM788	RM789	RM790	RM791	RM792	RM793	RM794	RM795	RM796	RM797	RM798	RM799	RM800	RM801	RM802	RM803	RM804	RM805	RM806	RM807	RM808	RM809	RM810	RM811	RM812	RM813	RM814	RM815	RM816	RM817	RM818	RM819	RM820	RM821	RM822	RM823	RM824	RM825	RM826	RM827	RM828	RM829	RM830	RM831	RM832	RM833	RM834	RM835	RM836	RM837	RM838	RM839	RM840	RM841	RM842	RM843	RM844	RM845	RM846	RM847	RM848	RM849	RM850	RM851	RM852	RM853	RM854	RM855	RM856	RM857	RM858	RM859	RM860	RM861	RM862	RM863	RM864	RM865	RM866	RM867	RM868	RM869	RM870	RM871	RM872	RM873	RM874	RM875	RM876	RM877	RM878	RM879	RM880	RM881	RM882	RM883	RM884	RM885	RM886	RM887	RM888	RM889	RM890	RM891	RM892	RM893	RM894	RM895	RM896	RM897	RM898	RM899	RM900	RM901	RM902	RM903	RM904	RM905	RM906	RM907	RM908	RM909	RM910	RM911	RM912	RM913	RM914	RM915	RM916	RM917	RM918	RM919	RM920	RM921	RM922	RM923	RM924	RM925	RM926	RM927	RM928	RM929	RM930	RM931	RM932	RM933	RM934	RM935	RM936	RM937	RM938	RM939	RM940	RM941	RM942	RM943	RM944	RM945	RM946	RM947	RM948	RM949	RM950	RM951	RM952	RM953	RM954	RM955	RM956	RM957	RM958	RM959	RM960	RM961	RM962	RM963	RM964	RM965	RM966	RM967	RM968	RM969	RM970	RM971	RM972	RM973	RM974	RM975	RM976	RM977	RM978	RM979	RM980	RM981	RM982	RM983	RM984	RM985	RM986	RM987	RM988	RM989	RM990	RM991	RM992	RM993	RM994	RM995	RM996	RM997	RM998	RM999	RM1000	RM1001	RM1002	RM1003	RM1004	RM1005	RM1006	RM1007	RM1008	RM1009	RM1010	RM1011	RM1012	RM1013	RM1014	RM1015	RM1016	RM1017	RM1018	RM1019	RM1020	RM1021	RM1022	RM1023	RM1024	RM1025	RM1026	RM1027	RM1028	RM1029	RM1030	RM1031	RM1032	RM1033	RM1034	RM1035	RM1036	RM1037	RM1038	RM1039	RM1040	RM1041	RM1042	RM1043	RM1044	RM1045	RM1046	RM1047	RM1048	RM1049	RM1050	RM1051	RM1052	RM1053	RM1054	RM1055	RM1056	RM1057	RM1058	RM1059	RM1060	RM1061	RM1062	RM1063	RM1064	RM1065	RM1066	RM1067	RM1068	RM1069	RM1070	RM1071	RM1072	RM1073	RM1074	RM1075	RM1076	RM1077	RM1078	RM1079	RM1080	RM1081	RM1082	RM1083	RM1084	RM1085	RM1086	RM1087	RM1088	RM1089	RM1090	RM1091	RM1092	RM1093	RM1094	RM1095	RM1096	RM1097	RM1098	RM1099	RM1100	RM1101	RM1102	RM1103	RM1104	RM1105	RM1106	RM1107	RM1108	RM1109	RM1110	RM1111	RM1112	RM1113	RM1114	RM1115	RM1116	RM1117	RM1118	RM1119	RM1120	RM1121	RM1122	RM1123	RM1124	RM1125	RM1126	RM1127	RM1128	RM1129	RM1130	RM1131	RM1132	RM1133	RM1134	RM1135	RM1136	RM1137	RM1138	RM1139	RM1140	RM1141	RM1142	RM1143	RM1144	RM1145	RM1146	RM1147	RM1148	RM1149	RM1150	RM1151	RM1152	RM1153	RM1154	RM1155	RM1156	RM1157	RM1158	RM1159	RM1160	RM1161	RM1162	RM1163	RM1164	RM1165	RM1166	RM1167	RM1168	RM1169	RM1170	RM1171	RM1172	RM1173	RM1174	RM1175	RM1176	RM1177	RM1178	RM1179	RM1180	RM1181	RM1182	RM1183	RM1184	RM1185	RM1186	RM1187	RM1188	RM1189	RM1190	RM1191	RM1192	RM1193	RM1194	RM1195	RM1196	RM1197	RM1198	RM1199	RM1200	RM1201	RM1202	RM1203	RM1204	RM1205	RM1206	RM1207	RM1208	RM1209	RM1210	RM1211	RM1212	RM1213	RM1214	RM1215	RM1216	RM1217	RM1218	RM1219	RM1220	RM1221	RM1222	RM1223	RM1224	RM1225	RM1226	RM1227	RM1228	RM1229	RM1230	RM1231	RM1232	RM1233	RM1234	RM1235	RM1236	RM1237	RM1238	RM1239	RM1240	RM1241	RM1242	RM1243	RM1244	RM1245	RM1246	RM1247	RM1248	RM1249	RM1250	RM1251	RM1252	RM1253	RM1254	RM1255	RM1256	RM1257	RM1258	RM1259	RM1260	RM1261	RM1262	RM1263	RM1264	RM1265	RM1266	RM1267	RM1268	RM1269	RM1270	RM1271	RM1272	RM1273	RM1274	RM1275	RM1276	RM1277	RM1278	RM1279	RM1280	RM1281	RM1282	RM1283	RM1284	RM1285	RM1286	RM1287	RM1288	RM1289	RM1290	RM1291	RM1292	RM1293	RM1294	RM1295	RM1296	RM1297	RM1298	RM1299	RM1300	RM1301	RM1302	RM1303	RM1304	RM1305	RM1306	RM1307	RM1308	RM1309	RM1310	RM1311	RM1312	RM1313	RM1314	RM1315	RM1316	RM1317	RM1318	RM1319	RM1320	RM1321	RM1322	RM1323	RM1324	RM1325	RM1326	RM1327	RM1328	RM1329	RM1330</
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DBSNP	ALLELE1	ALLELE2	COMPARISON	RR	RR2	SIZE	FRQ1_A	FRQ2_A	SIZE_B	FRQ1_B	FRQ2_B
11448	G	A	HELD_FEM_ADR	0,73	1,38	69	99	39	68	114	22
11448	G	A	HELD_ALL_ADR	0,79	1,27	127	190	64	124	207	41
11448	G	A	HELD_ALL_CC	0,75	1,34	44	62	26	40	66	14
11450	T	A	HELD_MAL_LIP	0,42	2,37	19	21	17	36	61	11
11456	A	G	CVD_FEM	0,48	2,11	34	59	9	40	79	1
11462	G	T	HELD_MAL_LIP2	0,79	1,27	317	566	68	350	653	47
11462	G	T	HELD_ALL_LIP2	0,87	1,15	635	1142	128	735	1355	115
11483	T	C	HELD_FEM_ADR5ULN	0,41	2,41	17	30	4	69	133	5
11483	T	C	HELD_FEM_ADR3ULN	0,54	1,84	31	56	6	69	133	5
11483	T	C	HELD_FEM_ADR	0,73	1,36	73	135	11	69	133	5
11531	G	A	HELD_FEM_CC	0,64	1,56	31	47	15	22	41	3
11536	C	G	HELD_ALL_CC	0,95	1,06	43	66	20	40	63	17
11537	A	G	HELD_MAL_ADR	0,76	1,32	63	93	33	60	101	19
11558	A	C	HELD_MAL_LIP2	0,82	1,22	313	502	124	347	596	98
11558	A	C	HELD_ALL_LIP2	0,86	1,16	633	1036	230	722	1239	205
11558	A	C	HELD_ALL_CC	1,48	0,68	45	81	9	40	65	15
11585	G	T	HELD_MAL_CC	2,35	0,43	14	22	6	18	17	19
11594	T	C	HELD_ALL_ADR3ULN	5,88	0,17	46	91	1	127	234	20
11594	T	C	HELD_MAL_ADR	2,29	0,44	61	119	3	58	106	10
11614	T	C	HELD_FEM_CC	1,52	0,66	31	52	10	22	30	14
11614	T	C	HELD_MAL_CC2	1,49	0,67	48	84	12	29	43	15
11614	T	C	HELD_ALL_CC	1,24	0,8	45	74	16	40	60	20

SNP	ALLELE1	ALLELE2	COMPARISON	RR	SIZE	INFO A	INFO A	INFO A	INFO A	INFO B	INFO B
11614	T	C	HELD_ALL_HDL	1,02	0,98	45	76	14	59	99	19
11631	G	A	HELD_MAL_ADR5ULN	0,35	2,9	9	8	10	59	87	31
11631	G	A	HELD_MAL_ADR3ULN	0,55	1,82	17	19	15	59	87	31
11637	A	C	HELD_FEM_LIP	0,77	1,29	77	101	53	79	121	37
11637	A	C	HELD_ALL_LIP	0,76	1,31	96	123	69	114	171	57
11637	A	C	CVD_MAL	1,32	0,76	69	111	27	34	45	23
11637	A	C	CVD_ALL	1,28	0,78	105	169	41	74	104	44
11641	G	C	HELD_MAL_ADR	1,22	0,82	60	74	46	57	59	55
11645	G	A	HELD_FEM_CC	2,45	0,41	31	60	2	22	38	6
11646	C	T	HELD_FEM_LIP	1,31	0,77	81	122	40	79	102	56
11646	C	T	HELD_ALL_LIP	1,27	0,79	100	150	50	115	152	78
11652	C	T	HELD_MAL_LIP	1,02	0,98	19	22	16	35	40	30
11727	G	A	HELD_ALL_ADR5ULN	0	null	20	0	40	104	170	38
11727	G	A	HELD_MAL_ADR3ULN	0	null	13	0	26	46	68	24
11727	G	A	HELD_MAL_ADR5ULN	0	null	8	0	16	46	68	24
11727	G	A	HELD_ALL_ADR3ULN	3,06	0,33	37	70	4	104	170	38
11727	G	A	HELD_FEM_ADR5ULN	0	null	12	0	24	58	102	14
11728	T	C	HELD_ALL_ADR5ULN	2,43	0,41	24	44	4	128	205	51
11914	A	T	HELD_MAL_ADR3ULN	0,47	2,12	15	10	20	56	63	49
11938	T	C	HELD_ALL_ADR3ULN	1,17	0,85	48	64	32	132	163	101
11938	T	C	HELD_ALL_ADR5ULN	1,06	0,94	26	33	19	132	163	101
11938	T	C	HELD_FEM_ADR3ULN	1,11	0,9	31	38	24	72	83	61

HAZSP	ALLELE1	ALLELE2	COMPARISON	RR	RR2	SIZE A	FRQ1 A	FRQ2 A	SIZE B	FRQ1 B	FRQ2 B
12399	A	G	HELD_MAL_ADR5ULN	0,36	2,8	8	11	5	60	106	14
12399	A	G	HELD_MAL_ADR3ULN	0,51	1,97	16	24	8	60	106	14
12399	A	G	HELD_ALL_ADR	0,79	1,26	132	217	47	131	232	30
12554	A	T	HELD_MAL_ADR	0,71	1,41	62	98	26	55	99	11
12554	A	T	HELD_FEM_VEFF	0,82	1,23	151	234	68	144	243	45
12851	T	C	HELD_FEM_ADR5ULN	0,52	1,92	17	22	12	71	115	27
12851	T	C	HELD_MAL_ADR	1,07	0,94	62	94	30	60	88	32
13025	A	C	HELD_MAL_ADR3ULN	1,06	0,94	17	24	10	58	80	36
13025	A	C	HELD_FEM_ADR5ULN	0,7	1,43	17	19	15	70	93	47
13191	G	A	HELD_ALL_CC	0,72	1,39	43	50	36	39	58	20
13192	T	C	HELD_MAL_ADR3ULN	0,68	1,46	17	25	9	59	97	21
13192	T	C	HELD_MAL_ADR5ULN	0,79	1,27	9	14	4	59	97	21
13192	T	C	HELD_ALL_ADR3ULN	0,99	1,01	47	77	17	129	212	46
13192	T	C	HELD_MAL_ADR	0,94	1,06	61	98	24	59	97	21
13193	G	A	HELD_MAL_ADR3ULN	0,68	1,48	16	23	9	58	94	22
13193	G	A	HELD_MAL_ADR5ULN	0,74	1,36	8	12	4	58	94	22
13193	G	A	HELD_ALL_ADR3ULN	1,02	0,98	47	77	17	130	212	48
13338	G	A	HELD_FEM_VEFF	1,09	0,92	55	75	35	71	92	50
13338	G	A	HELD_FEM_VEFF	0,98	1,02	148	187	109	139	178	100
13339	G	A	HELD_MAL_ADR	0,9	1,11	50	42	58	50	47	53
13339	G	A	CVD_FEM	1,92	0,52	31	57	5	35	56	14
13340	C	A	HELD_FEM_VEFF	0,58	1,71	21	21	21	17	27	7

BAYSNP	ALLELE1	ALLELE2	COMPARISON	RR1	RR2	SIZE_A	TRFQ1_A	TRFQ1_B	SIZE_B	TRFQ1_B	TRFQ2_B
13479	G	A	HELD_FEM_UEFF	0,68	1,47	48	73	23	65	113	17
13633	T	C	HELD_FEM_ADR3ULN	0,59	1,68	27	36	18	69	112	26
13633	T	C	HELD_FEM_ADR	0,75	1,33	64	90	38	69	112	26
13929	G	A	HELD_MAL_ADR5ULN	0	null	8	0	16	54	94	14
14065	C	T	HELD_FEM_EFF	0,81	1,23	267	473	61	271	501	41
14083	T	C	HELD_FEM_ADR	1,5	0,67	69	123	15	70	112	28
14085	T	C	HELD_FEM_EFF	0,87	1,14	240	405	75	230	404	56
14087	T	C	HELD_FEM_EFF	0,87	1,14	268	452	84	283	496	70
14102	C	T	HELD_MAL_ADR5ULN	1,1	0,91	9	12	6	56	72	40
14102	C	T	HELD_FEM_EFF	1,15	0,87	271	361	181	281	340	222
14103	C	T	HELD_FEM_EFF	0,85	1,18	264	445	83	273	482	64
14103	C	T	HELD_FEM_VEFF	0,92	1,09	137	234	40	135	236	34
14103	C	T	HELD_FEM_UEFF	0,73	1,38	53	84	22	69	121	17
14129	A	G	HELD_ALL_ADR3ULN	0,77	1,29	47	53	41	116	151	81
14129	A	G	HELD_MAL_ADR3ULN	0,74	1,35	16	18	14	55	72	38
14326	A	C	HELD_FEM_EFF	1,18	0,85	272	454	90	285	449	121
14503	C	T	HELD_ALL_ADR5ULN	1,14	0,88	24	34	14	114	154	74
14503	C	T	HELD_ALL_ADR3ULN	0,91	1,1	45	58	32	114	154	74
14503	C	T	HELD_FEM_ADR5ULN	0,99	1,01	16	21	11	57	75	39
14503	C	T	HELD_FEM_ADR3ULN	0,86	1,17	29	35	23	57	75	39
14537	C	T	HELD_ALL_ADR	0,77	1,29	118	133	103	113	156	70
14537	C	T	HELD_FEM_ADR	0,77	1,29	67	68	66	59	76	42

HAYSNP	AE/ELEM1	ALLELEM2	COMPARISON	RR1	RR2	SIZE	FREQ1 A	FREQ2 A	SIZE B	FREQ1 B	FREQ2 B
15915	T	C	HELD_FEM_ADR	1,07	0,94	63	95	31	55	80	30
15915	T	C	HELD_ALL_ADR	1,08	0,92	111	172	50	106	158	54
15915	T	C	HELD_ALL_ADR3ULN	1,89	0,53	38	66	10	106	158	54
19289	G	A	HELD_MAL_CC	0,56	1,8	12	20	4	18	34	2
19289	G	A	HELD_ALL_CC	0,72	1,38	43	71	15	40	73	7
19289	G	A	HELD_MAL_LIP	0,57	1,75	19	27	11	34	59	9
36958	C	G	HELD_MAL_ADR3ULN	null	0	15	30	0	57	104	10
37158	C	A	HELD_ALL_ADR	0,79	1,27	122	139	105	114	157	71
37158	C	A	HELD_FEM_ADR	0,78	1,29	66	70	62	58	77	39
37160	C	T	HELD_FEM_UERF	0,65	1,54	53	86	20	73	133	13
37412	T	G	HELD_FEM_ADR5ULN	0,6	1,68	17	19	15	69	98	40
37412	T	G	HELD_ALL_ADR5ULN	0,69	1,46	26	32	20	129	185	73
37412	T	G	HELD_FEM_ADR3ULN	0,65	1,53	31	35	27	69	98	40
37457	T	A	CVD_ALL	2,53	0,4	53	101	5	28	43	13
37457	T	A	CVD_FEM	5,5	0,18	17	33	1	18	27	9
37457	T	A	CVD_MAL	1,62	0,62	36	68	4	10	16	4
37704	C	T	HELD_MAL_ADR5ULN	0,12	8,06	9	17	1	60	120	0
38959	C	A	CVD_ALL	0,94	1,06	57	99	15	31	55	7
38959	C	A	HELD_FEM_EFF	1,2	0,83	282	526	38	280	508	52
39292	G	A	HELD_FEM_ADR5ULN	0,38	2,61	9	12	6	47	82	12
39292	G	A	HELD_ALL_ADR5ULN	0,49	2,04	17	26	8	86	153	19
39698	T	C	HELD_MAL_ADR3ULN	0,67	1,5	16	13	19	56	60	52

SNP	ALLELE1	ALLELE2	COMPARISON	REF	REF	SIZE	FRQ1	FRQ2	SIZE B	FRQ1 B	FRQ2 B
39756	T	C	HELD_FEM_ADR3ULN	1,85	0,54	19	29	9	44	51	37
39951	T	C	HELD_MAL_ADR	1,24	0,81	52	78	26	54	72	36
39951	T	C	HELD_ALL_ADR	0,96	1,04	117	161	73	113	159	67
39951	T	C	HELD_FEM_ADR	0,81	1,23	65	83	47	59	87	31
39951	T	C	HELD_FEM_ADR3ULN	0,5	2,01	14	15	13	59	87	31
40466	G	T	HELD_FEM_EFF	1,31	0,76	266	469	63	266	436	96
40466	G	T	HELD_FEM_UEFF	1,62	0,62	52	93	11	69	110	28
40466	G	T	HELD_FEM_VEFF	1,32	0,76	139	244	34	135	219	51
44442	A	G	HELD_MAL_ADR3ULN	0,41	2,45	9	8	10	59	82	36
55504	T	C	HELD_MAL_ADR	1,33	0,75	60	75	45	56	54	58
55542	C	A	HELD_FEM_ADR	0,75	1,33	65	62	68	69	85	53
55670	C	T	HELD_FEM_VEFF	1,62	0,62	154	297	11	138	254	22
55736	A	G	HELD_ALL_ADR3ULN	null	0	15	30	0	87	147	27
55736	A	G	HELD_MAL_ADR3ULN	null	0	7	14	0	43	71	15
55736	A	G	HELD_FEM_ADR3ULN	null	0	8	16	0	44	76	12
55748	T	C	HELD_MAL_ADR3ULN	0	null	8	0	16	56	98	14
55813	T	C	HELD_ALL_ADR3ULN	0,66	1,51	44	39	49	119	139	99
55845	C	A	HELD_FEM_VEFF	0,81	1,24	136	152	120	135	179	91
55845	C	A	HELD_MAL_ADR3ULN	2,11	0,47	16	25	7	58	68	48
55845	C	A	HELD_FEM_UEFF	0,74	1,35	52	58	46	68	93	43
55923	C	T	HELD_FEM_ADR	0,74	1,35	59	63	55	57	78	36
55923	C	T	HELD_FEM_ADR3ULN	0,6	1,67	27	27	27	57	78	36

DBSNP	ALLELE1	ALLELE2	COMPARISON	RR	RR	SIZE A	FRQ A	FRQ2 A	SIZE B	FRQ1 B	FRQ2 B
56780	G	A	HBLD_ALL_ADR3ULN	0,61	1,65	36	28	44	94	105	83
56780	G	A	HBLD_ALL_ADR	0,83	1,21	105	96	114	94	105	83
56876	T	C	HBLD_FEM_UFFF	1,91	0,52	57	106	8	74	123	25
56876	T	C	HBLD_FEM_HFF	1,29	0,77	285	524	46	274	480	68
56876	T	C	HBLD_FEM_VFFF	1,42	0,71	154	285	23	143	248	38
56978	A	G	HBLD_ALL_ADR5ULN	2,13	0,47	26	42	10	124	157	91
57000	A	T	HBLD_FEM_VFFF	0,93	1,08	150	206	94	143	206	80
57000	A	T	HBLD_FEM_UFFF	1,03	0,97	54	76	32	75	104	46
57000	A	T	CVD_ALL	1,3	0,77	57	91	23	32	43	21
57000	A	T	CVD_MAL	1,23	0,82	39	64	14	13	18	8
57313	T	C	HBLD_FEM_UFFF	0,79	1,26	55	65	45	76	104	48
57734	C	G	HBLD_FEM_ADR3ULN	0,61	1,63	30	45	15	67	116	18
57837	A	G	HBLD_MAL_ADR3ULN	3,15	0,32	15	28	2	53	83	23
57853	T	C	HBLD_FEM_HFF	1,26	0,79	265	457	73	265	425	105
57853	T	C	HBLD_FEM_UFFF	1,62	0,62	52	91	13	68	104	32
57853	T	C	HBLD_FEM_VFFF	1,26	0,79	139	238	40	135	214	56
57854	G	A	HBLD_FEM_HFF	1,17	0,86	267	451	83	262	420	104
57854	G	A	HBLD_FEM_UFFF	1,52	0,66	52	90	14	68	104	32
57854	G	A	HBLD_MAL_ADR3ULN	2,61	0,38	16	29	3	57	86	28
58295	A	G	HBLD_MAL_ADR	0,78	1,29	56	48	64	54	60	48
58402	T	C	HBLD_MAL_ADR3ULN	0,49	2,04	17	10	24	56	57	55
58407	G	T	HBLD_FEM_VFFF	1,04	0,97	153	195	111	145	180	110

STRAYNR	ALLELE1	ALLELE2	COMPARISON	DIFF	ERR	SIZE	FREQ. A	FREQ. A	SIZE B	FREQ. B	FREQ. B
58407	G	T	HELD_FEM_UEFF	1,23	0,82	56	76	36	76	91	61
58440	T	C	HELD_FEM_UEFF	0,68	1,48	52	81	23	72	127	17
58525	C	T	HELD_FEM_ADR	0,55	1,83	66	110	22	66	128	4
58525	C	T	HELD_FEM_ADR3ULN	0,38	2,65	30	49	11	66	128	4
58525	C	T	HELD_FEM_ADR5ULN	0,28	3,55	16	26	6	66	128	4
58525	C	T	HELD_ALL_ADR	0,7	1,44	124	212	36	122	228	16
58525	C	T	HELD_ALL_ADR5ULN	0,47	2,14	25	42	8	122	228	16
58525	C	T	HELD_ALL_ADR3ULN	0,56	1,8	47	80	14	122	228	16
58533	C	T	HELD_FEM_ADR	0,59	1,69	67	114	20	71	136	6
58533	C	T	HELD_FEM_ADR3ULN	0,44	2,26	27	46	8	71	136	6
58533	C	T	HELD_FEM_ADR5ULN	0,38	2,67	14	24	4	71	136	6
58533	C	T	HELD_ALL_ADR	0,77	1,31	125	217	33	129	238	20
58544	G	A	HELD_MAL_ADR5ULN	0	null	6	0	12	54	85	23
58716	T	C	HELD_MAL_ADR3ULN	6,23	0,16	16	30	2	59	76	42
58716	T	C	HELD_MAL_ADR5ULN	3,42	0,29	8	14	2	59	76	42
58736	C	T	HELD_FEM_EFF	1,17	0,85	289	395	183	281	344	218
58808	A	G	HELD_FEM_ADR	1,34	0,75	68	100	36	61	74	48
58809	C	A	HELD_MAL_ADR5ULN	0	null	9	0	18	59	96	22
58809	C	A	HELD_ALL_ADR3ULN	0,7	1,42	46	70	22	128	215	41
58809	C	A	HELD_MAL_ADR3ULN	0,67	1,5	16	23	9	59	96	22
58809	C	A	HELD_FEM_UEFF	1,53	0,65	54	94	14	75	116	34
58886	A	G	HELD_FEM_ADR3ULN	0,57	1,76	31	20	42	72	74	70

RAYSONT	ALLELE1	ALLELE2	COMPARISON	REF	REF	SIZE	FRBO1	FRBO2	SIZE	FRBO1	FRBO2	SIZE	FRBO1	FRBO2	SIZE	FRBO1	FRBO2
58886	A	G	HELD_ALL_ADR3ULN	0,66	1,53	48	38	58	132	142	122	122	142	122	122	142	122
58886	A	G	HELD_ALL_ADR5ULN	0,59	1,68	26	20	32	132	142	122	122	142	122	122	142	122
58926	C	T	HELD_MAL_ADR3ULN	0,39	2,56	15	12	18	54	75	33	33	75	33	33	75	33
58926	C	T	HELD_ALL_ADR5ULN	0,5	2	22	19	25	113	144	82	82	144	82	82	144	82
58926	C	T	CVD_FEM	1,07	0,94	18	21	15	19	21	17	17	21	17	17	21	17
58926	C	T	HELD_MAL_ADR5ULN	0,4	2,51	8	7	9	54	75	33	33	75	33	33	75	33
58968	A	G	HELD_ALL_ADR5ULN	0,44	2,27	22	21	23	118	168	68	68	168	68	68	168	68
58968	A	G	HELD_MAL_ADR3ULN	0,4	2,52	13	12	14	55	81	29	29	81	29	29	81	29
58968	A	G	HELD_ALL_ADR3ULN	0,64	1,55	41	47	35	118	168	68	68	168	68	68	168	68
58968	A	G	HELD_FEM_ADR5ULN	0,47	2,14	14	13	15	63	87	39	39	87	39	39	87	39
58985	G	A	HELD_ALL_ADR5ULN	0,52	1,93	26	28	24	130	188	72	72	188	72	72	188	72
59113	C	G	HELD_MAL_ADR5ULN	0,13	7,7	8	2	14	55	64	46	46	64	46	46	64	46
59113	C	G	HELD_MAL_ADR3ULN	0,42	2,39	16	10	22	55	64	46	46	64	46	46	64	46
59236	G	A	HELD_ALL_ADR	0,83	1,21	95	103	87	96	122	70	70	122	70	70	122	70
59236	G	A	HELD_ALL_ADR3ULN	0,83	1,21	34	39	29	96	122	70	70	122	70	70	122	70
59236	G	A	HELD_FEM_ADR	0,78	1,29	52	47	57	51	59	43	43	59	43	43	59	43
59237	C	T	HELD_FEM_VEFF	1	1	121	140	102	119	138	100	100	138	100	100	138	100
59237	C	T	HELD_FEM_EFF	1,04	0,96	240	290	190	243	285	201	201	285	201	201	285	201
59267	T	C	HELD_FEM_VEFF	0,64	1,55	50	52	48	68	96	40	40	96	40	40	96	40
59352	T	C	HELD_MAL_ADR	0,94	1,07	58	73	43	56	74	38	38	74	38	38	74	38
59352	T	C	HELD_ALL_ADR	1,01	0,99	126	167	85	125	164	86	86	164	86	86	164	86
59363	T	C	CVD_MAL	1,27	0,79	60	84	36	28	30	26	26	30	26	26	30	26

2BAYSNP	ALLELE1	ALLELE2	COMPARISON	OR	PR	SIZE	FREQ1	FREQ2	SIZE B	FREQ B	FREQ2 B
59368	T	C	HELD_FEM_ADR	0,7	1,42	66	74	58	69	100	38
59371	C	T	HELD_FEM_VEFF	0,89	1,13	141	153	129	136	164	108
59371	C	T	HELD_FEM_UVEFF	0,85	1,18	52	60	44	68	88	48
59372	C	T	HELD_MAL_ADR	0,69	1,44	55	87	23	58	104	12
59372	C	T	HELD_MAL_ADR3ULN	0,5	2	17	26	8	58	104	12
59443	T	C	HELD_ALL_ADR5ULN	1,32	0,75	19	25	13	95	110	80
59443	T	C	HELD_MAL_ADR5ULN	0,93	1,08	7	7	7	45	47	43
900080	G	C	HELD_FEM_ADR3ULN	0,47	2,12	31	52	10	71	135	7
900080	G	C	HELD_FEM_ADR5ULN	0,42	2,36	17	29	5	71	135	7
900102	T	G	HELD_FEM_UVEFF	1,55	0,65	55	73	37	78	76	80
900102	T	G	HELD_FEM_VEFF	1,23	0,82	153	204	102	147	168	126
900111	G	A	HELD_FEM_UVEFF	1,48	0,68	55	73	37	78	79	77
900111	G	A	HELD_FEM_VEFF	1,2	0,83	151	198	104	146	166	126
900117	T	G	HELD_MAL_LIP	3,44	0,29	17	31	3	33	44	22
900118	G	A	HELD_FEM_EFF	1,6	0,63	252	469	35	259	444	74
900118	G	A	HELD_FEM_VEFF	1,47	0,68	130	241	19	130	225	35
900118	G	A	HELD_FEM_ADR5ULN	1,12	0,89	15	28	2	59	109	9
900118	G	A	HELD_ALL_ADR5ULN	0,81	1,24	23	42	4	110	205	15
900120	T	C	HELD_FEM_EFF	1,28	0,78	286	511	61	280	471	89
900121	T	G	HELD_FEM_EFF	0,88	1,13	269	353	185	266	379	153
900123	A	G	HELD_ALL_ADR	null	0	119	238	0	115	226	4
900123	A	G	HELD_FEM_ADR	null	0	64	128	0	59	115	3

BAVSNP	ALLELE1	ALLELE2	COMPARISON	RRR	RRR2	SIZEA	FREQ1A	FREQ2A	SIZEB	FREQ1B	FREQ2B
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900132	T	C	HELD_FEM_ADR	1,21	0,83	67	111	23	58	89	27
900144	A	G	CVD_FEM	null	0	28	56	0	40	74	6
900144	A	G	HELD_ALL_ADR5ULN	null	0	26	52	0	125	240	10
900145	G	T	CVD_FEM	1,55	0,65	30	58	2	39	73	5
900145	G	T	HELD_ALL_ADR5ULN	null	0	25	50	0	121	232	10
900146	A	G	HELD_FEM_ADR5ULN	0,52	1,93	17	22	12	67	109	25
900146	A	G	HELD_FEM_CC	1,19	0,84	30	50	10	22	34	10
900146	A	G	HELD_MAL_ADR	1,21	0,82	58	97	19	54	84	24
900147	T	C	HELD_ALL_ADR3ULN	1,83	0,55	44	74	14	119	168	70
900147	T	C	HELD_FEM_ADR3ULN	2,12	0,47	28	48	8	66	91	41
900196	C	T	HELD_MAL_LIP	0,48	2,08	19	17	21	32	47	17
900196	C	T	HELD_FEM_LIP	2,71	0,37	12	19	5	36	37	35
900196	C	T	HELD_FEM_ADR3ULN	2,02	0,5	23	37	9	62	77	47
900196	C	T	CVD_FEM	1	1	6	8	4	15	20	10
900196	C	T	CVD_ALL	1,44	0,69	21	30	12	31	36	26
900200	T	C	CVD_FEM	0,58	1,71	20	23	17	38	58	18
900204	C	G	HELD_FEM_EFF	1,19	0,84	270	430	110	261	384	138
900205	C	G	HELD_FEM_EFF	0,9	1,12	283	364	202	274	380	168
900205	C	G	CVD_MAL	0,82	1,22	69	90	48	31	49	13
900223	G	A	HELD_FEM_ADR	3,59	0,28	43	85	1	31	57	5
900225	G	A	HELD_ALL_ADR5ULN	0	null	23	0	46	126	234	18

TRAYSNP	ALLELE1	ALLELE2	COMPARISON	NGF	RR	SIZE	FREQ1	FREQ2	SIZE	FREQ1	FREQ2	SIZE	FREQ1	FREQ2	FREQ3
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900227	A	C	HELD_FEM_ADR5ULN	5,9	0,17	17	33	1	72	118	26				
900233	T	A	HELD_FEM_ADR5ULN	1,39	0,72	17	23	11	72	84	60				
900236	C	T	HELD_FEM_ADR3ULN	0,6	1,68	31	50	12	69	125	13				
900236	C	T	HELD_MAL_ADR5ULN	null	0	9	18	0	60	104	16				
900241	C	G	HELD_FEM_EFF	0,97	1,03	276	367	185	275	373	177				
900242	G	C	HELD_ALL_ADR5ULN	0	null	26	0	52	132	220	44				
900242	G	C	HELD_ALL_ADR3ULN	4,65	0,21	48	93	3	132	220	44				
900242	G	C	HELD_FEM_ADR5ULN	0	null	17	0	34	72	119	25				
900242	G	C	HELD_MAL_ADR3ULN	0	null	17	0	34	60	101	19				
900242	G	C	HELD_FEM_ADR	1,87	0,54	73	136	10	72	119	25				
900242	G	C	HELD_FEM_ADR3ULN	3,09	0,32	31	59	3	72	119	25				
900242	G	C	HELD_ALL_ADR	1,42	0,7	136	246	26	132	220	44				
900242	G	C	HELD_MAL_ADR5ULN	0	null	9	0	18	60	101	19				

Claims

1. An isolated polynucleotide encoded by a phenotype associated (PA) gene; the polynucleotide is selected from the group comprising
 - 5 SEQ ID 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 10 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 15 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 20 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292 with allelic variation as indicated in the sequences section contained in a functional surrounding like full length cDNA for PA gene polypeptide and with or without the PA gene promoter 25 sequence.
2. An expression vector containing one or more of the polynucleotides of claim 1.
- 30 3. A host cell containing the expression vector of claim 2.

4. A substantially purified PA gene polypeptide encoded by a polynucleotide of claim 1.
5. A method for producing a PA gene polypeptide, wherein the method comprises the following steps:
 - a) culturing the host cell of claim 3 under conditions suitable for the expression of the PA gene polypeptide; and
 - 10 b) recovering the PA gene polypeptide from the host cell culture.
6. A method for the detection of a polynucleotide of claim 1 or a PA gene polypeptide of claim 4 comprising the steps of:
 - 15 contacting a biological sample with a reagent which specifically interacts with the polynucleotide or the PA gene polypeptide.
7. A method of screening for agents which regulate the activity of a PA gene comprising the steps of:
 - 20 contacting a test compound with a PA gene polypeptide encoded by any polynucleotide of claim 1; and detecting PA gene activity of the polypeptide, wherein a test compound which increases the PA gene polypeptide activity is identified as a potential therapeutic agent for increasing the activity of the PA gene polypeptide and wherein a test compound which decreases the PA
 - 25 activity of the polypeptide is identified as a potential therapeutic agent for decreasing the activity of the PA gene polypeptide.
8. A reagent that modulates the activity of a PA polypeptide or a polynucleotide wherein said reagent is identified by the method of the claim 7.

9. A pharmaceutical composition, comprising:
the expression vector of claim 2 or the reagent of claim 8 and a pharmaceutically acceptable carrier.
- 5 10. Use of the reagent according to claim 8 for the preparation of a medicament.
- 10 11. A method for determining whether a human subject has, or is at risk of developing a cardiovascular disease, comprising determining the identity of nucleotide variations as indicated in the sequences section of SEQ ID 1-292 of the PA gene locus of the subject and where the SNP class of the SNP is "CVD" as can be seen from table 3; whereas a "risk" genotype has a risk ratio of greater than 1 as can be seen from table 6.
- 15 12. A method for determining a patient's individual response to statin therapy, including drug efficacy and adverse drug reactions, comprising determining the identity of nucleotide variations as indicated in the sequences section of SEQ ID 1-292 of the PA gene locus of the subject and where the SNP class of the SNP is "ADR", "EFF" or both as can be seen from table 3; whereas the probability for such response can be seen from table 6.
- 20 13. Use of the method according to claim 12 for the preparation of a medicament tailored to suit a patient's individual response to statin therapy.
- 25 14. A kit for assessing cardiovascular status or statin response, said kit comprising
- 30 a) sequence determination primers and
- b) sequence determination reagents,

wherein said primers are selected from the group comprising primers that hybridize to polymorphic positions in human PA genes according to claim 1; and primers that hybridize immediately adjacent to polymorphic positions in human PA genes according to claim 1.

5

15. A kit as defined in claims 12 detecting a combination of two or more, up to all, polymorphic sites selected from the groups of sequences as defined in claim 1.

10

16. A kit for assessing cardiovascular status or statin response, said kit comprising one or more antibodies specific for a polymorphic position defined in claim 1 within the human PA gene polypeptides and combinations of any of the foregoing.

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JC20 Rec'd PCT/PTO 01 JUL 2005

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<223> baySNP533, T501C

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<223> baySNP542, T501C

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- 12 -

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<223> baySNP2186, T501C

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<223> baySNP2187, C501T

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<222> (501)..(501)

<223> baySNP2290, G501A

<400> 44

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<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP2327, A501C

<400> 45

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP2353, A501G

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<221> variation

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<223> baySNP2371, T501G

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- 30 -

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<223> baySNP2401, C501A

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<213> Homo Sapiens

<220>

<221> variation

- 31 -

<222> (501)..(501)

<223> baySNP2463, C501T

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<212> DNA

<213> Homo Sapiens

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<223> baySNP2755, A501G

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<210> 52

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<211> 1001

<212> DNA

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<223> baySNP2925, T501C

<400> 52

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<212> DNA

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<223> baySNP3152, T501A

<400> 54

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<211> 1001

<212> DNA

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<222> (501)..(501)

<223> baySNP3214, G501C

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<223> baySNP3215, G501C

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 <223> baySNP3241, C501T

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<221> variation

<222> (501)..(501)

<223> baySNP3826. T501G

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<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP3842, C501G

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<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP3843, A501T

<400> 61

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<223> baySNP3869, T501G

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<223> baySNP4206, A501T

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<222> (501)..(501)

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<223> baySNP4668, C501A

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<212> DNA

<213> Homo Sapiens

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<221> variation

<222> (501)..(501)

<223> baySNP4669, C501T

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<223> baySNP4718, C501T

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<222> (501)..(501)

<223> baySNP4818, A501G

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<222> (501)..(501)

<223> baySNP4827, T501C

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<222> (501)..(501)

<223> baySNP4838, A501G

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<222> (177) .. (177)

<223> baySNP4856, T177C

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<222> (501) .. (501)

<223> baySNP4868, C501T

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<223> baySNP4951, C501T

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<223> baySNP4966, A501G

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- 51 -

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<223> baySNP5278, T501C

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- 53 -

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<223> baySNP5569, T501C

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<223> baySNP5717, A501G

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- 60 -

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<223> baySNP6396, C501T

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<223> baySNP6524, T501C

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<223> baySNP6596, C501T

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<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP7128, C501T

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<211> 971

<212> DNA

<213> Homo Sapiens

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<222> (471)..(471)

<223> baySNP7363, C471T

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<211> 814

<212> DNA

<213> Homo Sapiens

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<221> variation

<222> (349)..(349)

<223> baySNP7409, A349G

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<223> baySNP8138, G501A
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<223> baySNP8168, A501C
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<221> variation

<222> (501)..(501)

<223> baySNP8210, C501T

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<212> DNA

<213> Homo Sapiens

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<220>

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<222> (501)..(501)

<223> baySNP8241, T501C

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP8249, G501A

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- 74 -

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<213> Homo Sapiens

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<223> baySNP8577, C501T

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<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP8578, A501G

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<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP8653, G501A

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<223> baySNP10091, G501A

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<223> baySNP10785, G501A

<400> 138

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<223> baySNP10811, T501C

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<223> baySNP10830, A501G

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<222> (501)..(501)

<223> baySNP10962, A501G

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<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP11000, C501T

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<212> DNA

<213> Homo Sapiens

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<223> baySNP11001, C501T

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- 89 -

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<223> baySNP11248, C501T

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<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP11410, G501T

<400> 150

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<223> baySNP11448, T501C

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<212> DNA

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<222> (501)..(501)

<223> baySNP11450, T501A

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<222> (501)..(501)

<223> baySNP11462, C501A

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP11483, G501A

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<223> baySNP11531, A501G

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<222> (501)..(501)

<223> baySNP11536, C501G

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<223> baySNP11537, T501C

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<222> (501)..(501)

<223> baySNP11558, T501G

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<223> baySNP11585, G501T

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<223> baySNP11614, C501T

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<221> variation

<222> (301)..(301)

<223> baySNP11631, A301G

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<222> (501)..(501)

<223> baySNP11637, A501C

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP11641, G501C

<400> 165

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<210> 166

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

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<223> baySNP11645, C501T

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- 101 -

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<222> (501)..(501)

<223> baySNP11646, A501G

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<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> variation

<222> (501)..(501)

<223> baySNP11652, C501T

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<211> 1001

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<213> Homo Sapiens

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<222> (501) .. (501)

<223> baySNP11727, A501G

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP11728, C501T

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<211> 1001

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<213> Homo Sapiens

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<221> variation

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<223> baySNP11914, T501A

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<212> DNA

<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP11938, G501A

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<212> DNA

<213> Homo Sapiens

<220>

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<222> (501)..(501)

<223> baySNP11950, T501C

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 ctttacacac tggtaaataa ataacggcat gtccctctt gttcctgtgg gtcaatcaac 180

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<212> DNA

<213> Homo Sapiens

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<223> baySNP13340,T501G

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- 122 -

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<223> baySNP38959,T501G

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<220>

<221> variation

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- 129 -

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<223> baySNP39951, T501C

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<220>

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<222> (366)..(366)

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- 131 -

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<223> baySNP55542, C501A

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<223> baySNP55670, G501A

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<223> baySNP55736, 501A

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<222> (501)..(501)

<223> baySNP55845, A501C

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<211> 1001

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP55923, C501T

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gatgaaatgg	accaaactac	accacagtga	catccaccag	tctacaaatt	ttactaggca	360
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<223> baySNP55945, C501T

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<223> baySNP56007, C482T

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<213> Homo Sapiens

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<223> baySNP56011, T501C

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<222> (501)..(501)

<223> baySNP56104, C501T

<400> 229

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<213> Homo Sapiens

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<223> baySNP56113, C501A

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<210> 231

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<212> DNA

<213> Homo Sapiens

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<223> baySNP56636, C501T

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<213> Homo Sapiens

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<223> Unsure

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<223> baySNP56666, A499G

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<212> DNA

<213> Homo Sapiens

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<220>

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<223> baySNP56667, C501T

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<223> baySNP57313, A501G

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<222> (501)..(501)

<223> baySNP57837, G501A

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<223> baySNP58525, C501T

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<213> Homo Sapiens

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<220>

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<222> (501)..(501)

<223> baySNP58533, T501C

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<223> baySNP58544, A501G

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<222> (501)..(501)

<223> baySNP58716, C501T

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<222> (501)..(501)

<223> baySNP58736, G501A

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<221> variation

<222> (501)..(501)

<223> baySNP58808, A501G

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<212> DNA

<213> Homo Sapiens

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<220>

<221> variation

<222> (295) .. (295)

<223> baySNP58809, T295G

<400> 253

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<210> 254

<211> 756

<212> DNA

<213> Homo Sapiens

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<222> (256) .. (256)

<223> baySNP58886, G256A

<400> 254

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<212> DNA

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<223> baySNP58926, G501A

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<221> variation

<222> (501) .. (501)

<223> baySNP58968, T501C

<400> 256

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<213> Homo Sapiens

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<221> variation

<222> (501)..(501)

<223> baySNP58985, C501T

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<220>

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<223> baySNP59113, G501C

<400> 258

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<212> DNA

<213> Homo Sapiens

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<223> baySNP59236, A501G

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<223> Unsure

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<223> baySNP59237. T501C

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<210> 261

<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP59267, C501T

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<210> 262

<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP59352, T501C

<400> 262

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attgcacaca	atcaaacata	ttaacttctt	aaacttctta	gtaactttcc	aaacaaatta	300

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<210> 263

<211> 1001

<212> DNA

<213> Homo Sapiens

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<221> variation

<222> (501)..(501)

<223> baySNP59363, C501T

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<212> DNA

<213> Homo Sapiens

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<223> baySNP59368, C501T

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP59371, C501T

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<213> Homo Sapiens

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<223> baySNP59372, C501T

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<213> Homo Sapiens

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<223> baySNP59443, G501A

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP900080, C501G

<400> 268

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<211> 862

<212> DNA

<213> Homo Sapiens

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<220>

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<222> (501)..(501)

<223> baySNP900102, C501A

<400> 269

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<221> variation

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<223> baySNP900111, T501C

<400> 270

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<223> Unsure

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<220>

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<223> baySNP900118, T501C

<400> 272

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<212> DNA

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<223> baySNP900120, G501A

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<212> DNA

<213> Homo Sapiens

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<222> (501)..(501)

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<222> (501)..(501)

<223> baySNP900124, G501A

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<212> DNA

<213> Homo Sapiens

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<223> baySNP900132, G501A

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<223> baySNP900144, A501G

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<212> DNA

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ctgttcrttc acccctttaa acaaatgctt tttcatgtgt tttatgatag gacccttate 960
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<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> variation

<222> (501)..(501)

<223> baySNP900147, G501A

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP900196, G501A

<400> 282

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tgtaagtaag	agtaactaaa	atatatatct	agaagttata	tacacactga	tttggccaaa	300
aaccctaaaa	agtattaaat	atacayatat	ttagttagta	aaaacaaacc	cctgtgtatt	360
gctaactact	tctgtaaaat	ttactcttca	gtagaaattc	atgttcaaga	gtcttcaatc	420
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gaagaaattg	tctcaacagt	ttgtgaatca	tatggaggtt	ttactaggct	ctttcctaag	600
gccacaaata	gtaatcagtt	tggttttgtg	taatatattc	tccaagcatg	cctagaggca	660
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<211> 841

<212> DNA

<213> Homo Sapiens

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<221> variation

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<223> baySNP900200, G501A

<400> 283

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tgtagaataa	cctctgctgt	ctacatactg	cagccccaaa	aaccagacct	cgcgcaaac	360
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atttagcggt	tcctccttgg	aagaatttta	caaataagac	atcaagttgg	tcacagagaa	780
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<210> 284

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> variation

<222> (501)..(501)

<223> baySNP900204, C501G

<400> 284

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ggtgatagat gaaatgaact gtatgaagat ccaccagcct ggcccacacg tggaagaagg      240
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tgaccagggc ttttgctatc coctgaecac ggtgctcatt gtccacagag agatgaaaca      420
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<210> 285

<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP900205, C501G

<400> 285

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atcatcaacg ggcagagctc ctactgtgcc caccaccttc tcttcagatt caaccaccca      240
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tgctatgtct acataccgcg tccaggggtt tttggcaagg aaccacaggg caggaaggag 360
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<210> 286

<211> 1001

<212> DNA

<213> Homo Sapiens

<220>

<221> variation

<222> (501)..(501)

<223> baySNP900223, A501G

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<210> 287

<211> 1001

<212> DNA

<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP900225, T501C

<400> 287

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<210> 288

<211> 1001

<212> DNA

<213> Homo Sapiens

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<223> baySNP900227, T501G

<400> 288

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aaccattggc agaaatgaat agttgtcttt gttacttaga agtattgtcc tctggaaaaa 960
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<211> 1001

<212> DNA

<213> Homo Sapiens

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<222> (501)..(501)

<223> baySNP900233, T501A

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 gtcttttcag acttattcag aatcttttcc aaatagaacc tcaagtttca caataaaaaa 420
 gaatgtggga ggggggagta gaaagtggag aaagagaagg agaagaaaaa gatgtattag 480
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<212> DNA

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<222> (501)..(501).

<223> baySNP900236, C501T

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<212> DNA

<213> Homo Sapiens

<220>

<221> variation

<222> (501)..(501)

<223> baySNP900241, C501G

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<211> 1001

<212> DNA

<213> Homo Sapiens

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<220>

<221> variation

<222> (501)..(501)

<223> baySNP900242, C501G

<400> 292

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gaagggtgaac	tgagacattg	acaacgtgca	agatgtggcc	aagtgggtggc	tgtttggtgg	720
gagtttggcc	aacgtgtgga	tgtgcatgct	cagggtgtcca	caagcatgta	aagggagccc	780
ctcacagtgt	tggatagagt	ggtagtggga	agagaaaggg	agtagcctca	accaggagct	840
gggggatgac	tatccaagtt	caagagtaga	actctgaaga	gtctaagaat	tttaaatttg	900
gacctaccct	tttggtcatt	aggaagttat	aattgcaaag	ctaggagaat	agagcacatt	960
tttatttaac	gtcttggtac	cttcattaaa	acttaaatat	t		1001

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(54) Title: **SINGLE NUCLEOTIDE POLYMORPHISMS AS PREDICTIVE DIAGNOSTICS FOR ADVERSE DRUG REAC-
TIONS (ADR) AND DRUG EFFICACY**

(57) Abstract: The invention provides diagnostic methods and kits including oligo and/or polynucleotides or derivatives, including as well antibodies determining whether a human subject is at risk of getting adverse drug reaction after statin therapy or whether the human subject is a high or low responder or a good or bad metabolizer of statins. The invention provides further diagnostic methods and kits including antibodies determining whether a human subject is at risk for a cardiovascular disease. Still further the invention provides polymorphic sequences and other genes.

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A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12Q1/68 G01N33/50 C07K14/47 C12N15/63 A61K48/00 A61K38/17		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12Q C07K A61K G01N C12N		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used) EPO-Internal, BIOSIS, EMBL, Sequence Search, WPI Data, PAJ		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DATABASE EMBL 'Online! 4 June 1995 (1995-06-04), HABETS ET AL.: "Human T-lymphoma invasion and metastasis inducing TIAM1 protein (TIAM1) mRNA, complete cds." XP002279808 Database accession no. HS162961 cited in the application the whole document ----- -/--	1-5,7,9
<input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. "B" document member of the same patent family		
Date of the actual completion of the international search 26 May 2004		Date of mailing of the international search report 26.08.04
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer Seroz, T

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/000539

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	HABETS G G M ET AL: "SEQUENCE OF THE HUMAN INVASION-INDUCING TIAM1 GENE, ITS CONSERVATION IN EVOLUTION AND ITS EXPRESSION IN TUMOR CELL LINES OF DIFFERENT TISSUE ORIGIN" ONCOGENE, BASINGSTOKE, HANTS, GB, vol. 10, no. 7, 6 April 1995 (1995-04-06), pages 1371-1376, XP002039499 ISSN: 0950-9232 figure 1	1-5,7,9
A	HWANG DAVID M ET AL: "A genome-based resource for molecular cardiovascular medicine: Toward a compendium of cardiovascular genes" CIRCULATION, AMERICAN HEART ASSOCIATION, DALLAS, TX, US, vol. 96, no. 12, 16 December 1997 (1997-12-16), pages 4146-4203, XP002197842 ISSN: 0009-7322 cited in the application tables 8,9	1-5,7,9, 11-16
A	EP 1 136 554 A (BAYER AG) 26 September 2001 (2001-09-26) claims 1-15; examples 1-4	1-5,7,9, 11-16
A	OHNISHI Y ET AL: "IDENTIFICATION OF 187 SINGLE NUCLEOTIDE POLYMORPHISMS (SNPS) AMONG 41 CANDIDATE GENES FOR ISCHEMIC HEART DISEASE IN THE JAPANESE POPULATION" HUMAN GENETICS, BERLIN, DE, vol. 106, 2000, pages 288-292, XP002949197 ISSN: 0340-6717 table 1	1-5,7,9, 11-16
A	TURNER S T ET AL: "Antihypertensive pharmacogenetics: Getting the right drug into the right patient" JOURNAL OF HYPERTENSION, CURRENT SCIENCE, PHILADELPHIA, PA, US, vol. 19, no. 1, January 2001 (2001-01), pages 1-11, XP002241062 ISSN: 0263-6352 page 4, paragraphs 2,3 page 7, paragraph 3 - page 8, right-hand column, last paragraph	1-5,7,9, 11-16

-/-

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP2004/000539

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>DORNBROOK-LAVENDER KIMBERLY A ET AL: "Genetic polymorphisms in emerging cardiovascular risk factors and response to statin therapy." CARDIOVASCULAR DRUGS AND THERAPY, vol. 17, no. 1, January 2003 (2003-01), pages 75-82, XP009030786 ISSN: 0920-3206 (ISSN print)</p>	

INTERNATIONAL SEARCH REPORT

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Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

a. type of material



a sequence listing



table(s) related to the sequence listing

b. format of material



in written format



in computer readable form

c. time of filing/furnishing



contained in the international application as filed



filed together with the international application in computer readable form



furnished subsequently to this Authority for the purpose of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

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PCT/EP2004/000539

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claim 11 and 12 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 6, 8, 9 (partially), 10
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-16 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.1

Although claim 11 and 12 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box II.2

Claims Nos.: 6, 8, 9 (partially), 10

Present claims 6, 8-10 relate to a product (reagent) defined by reference to a desirable characteristic or property, namely its ability to bind to a polypeptide according to the present application and modulate the activity of said polypeptide.

The claims cover all reagents having this characteristic or property, whereas the application does not provide any support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for such reagents. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the reagents by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, no search has been carried out for claims 6, 8 and 10, and claim 9 has been searched with respect to the expression vector of claim 2.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP2004/000539

Patent document cited in search report		Publication date		Patent family member(s)	Publication date
EP 1136554	A	26-09-2001	EP	1136554 A1	26-09-2001
			AU	4419601 A	03-10-2001
			WO	0170810 A2	27-09-2001
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